



Db 7103 TGCCTCCGAAGCCATAGAAAGTTGCAAAATCCCGGCACTGAGAAAGAAAACACGCTC 7162  
Qy 61 TTGAATTTCTTGAAGTACCTCTTAATTCATTCATGCTGACCTCCGAGATGTAGTAG 120  
Db 7163 TTGAATTTCTTGAAGTACCTCTTAATTCATTCATGCTGACCTCCGAGATGTAGTAG 7222  
Qy 121 CTGACTCATTAATTCACAGGTGTTATGTCTACCCATTCACCTGCAACATGAATTAAGTG 180  
Db 7223 CTGACTCATTAATTCACAGGTGTTATGTCTACCCATTCACCTGCAACATGAATTAAGTG 7282  
Qy 181 ATTCTGAAACCACTGCCCCCTAGGGGAACTACAAGGTTAGATTCCCGTACGCTCTGCTCA 240  
Db 7283 ATTCTGAAACCACTGCCCCCTAGGGGAACTACAAGGTTAGATTCCCGTACGCTCTGCTCA 7342  
Qy 241 CGTTTGTGTTAACAATCAATTAATTAATACCTTGTGTTGTGCTCATTTCTGTTTAAATAT 300  
Db 7343 CGTTTGTGTTAACAATCAATTAATTAATACCTTGTGTTGTGCTCATTTCTGTTTAAATAT 7402  
Qy 301 CTTTATTTAATAGCACTGCTTAATTTCTTCAACATTTGGTTCAACAACCAAAAGGCCCTATT 360  
Db 7403 CTTTATTTAATAGCACTGCTTAATTTCTTCAACATTTGGTTCAACAACCAAAAGGCCCTATT 7462  
Qy 361 AACTGGAAGCCCTGAATGAAGCTTACATTAACAACAATGTTTCTTATAGAGAAAATTT 420  
Db 7463 AACTGGAAGCCCTGAATGAAGCTTACATTAACAACAATGTTTCTTATAGAGAAAATTT 7522  
Qy 421 TTCTTCAATCTGCTCCACAGCCCTTCTGCTTAAATGTGGAACAATATATCATPACTG 480  
Db 7523 TTCTTCAATCTGCTCCACAGCCCTTCTGCTTAAATGTGGAACAATATATCATPACTG 7582  
Qy 481 AAATGCACTATTTAATCTGATTTTAACTGTAAGTCAAGTCAAGTCAATTAAGTCACTTAC 540  
Db 7583 AAATGCACTATTTAATCTGATTTTAACTGTAAGTCAAGTCAAGTCAATTAAGTCACTTAC 7642  
Qy 541 CTGCTGTGAAATATGATCAACATTCATCTAGAACTTTTGTATCTTCTGCAATGAA 600  
Db 7643 CTGCTGTGAAATATGATCAACATTCATCTAGAACTTTTGTATCTTCTGCAATGAA 7702  
Qy 601 AACTGTGATCTTATGCAACATGAGCTTTCCCAATCAACAACCGACCTTCTCCAGCCCC 660  
Db 7703 AACTGTGATCTTATGCAACATGAGCTTTCCCAATCAACAACCGACCTTCTCCAGCCCC 7762  
Qy 661 CCGGACACACATCTCTTCCATGACATGCAATCTGCTGCTGGAACAAGGCCCTTCA 720  
Db 7763 CCGGACACACATCTCTTCCATGACATGCAATCTGCTGCTGGAACAAGGCCCTTCA 7822  
Qy 721 ACACTAGCTTGGGGGCACTGTAGCAACAGATCACTCCCTACCGGCAACCAATGCA 780  
Db 7823 ACACTAGCTTGGGGGCACTGTAGCAACAGATCACTCCCTACCGGCAACCAATGCA 7882  
Qy 781 ACAAAAATATTAAGCAATGCTGATTCGATTCGAAAAAGGCTGCTTGAAGTGA 840  
Db 7883 ACAAAAATATTAAGCAATGCTGATTCGATTCGATTCGAAAAAGGCTGCTTGAAGTGA 7942  
Qy 841 GGGGTGAAGCAAGGCAAGAAATTAAGTGAAGTGAACCTGAGTGGAGTCCGTGTGTTGA 900  
Db 7943 GGGGTGAAGCAAGGCAAGAAATTAAGTGAAGTGAACCTGAGTGGAGTCCGTGTGTTGA 8002  
Qy 901 AGCTCAAAATTTTCCATTTGCTGTGCAATGCAAAATGCTTATTAAGCACTGTAAAG 960  
Db 8003 AGCTCAAAATTTTCCATTTGCTGTGCAATGCAAAATGCTTATTAAGCACTGTAAAG 8062  
Qy 961 ATTGATTAATGAAGTGAATGAATATCTGCAAGAACATTAATGTGCAAGGAGATCAT 1020  
Db 8063 ATTGATTAATGAAGTGAATGAATATCTGCAAGAACATTAATGTGCAAGGAGATCAT 8122  
Qy 1021 GAATTAAGAGCACTGACATGTGGAATGAATATCTTGTTCCTTTATTCAGAGCTGA 1080  
Db 8123 GAATTAAGAGCACTGACATGTGGAATGAATATCTTGTTCCTTTATTCAGAGCTGA 8182  
Qy 1081 AGGAGAAAGGCTCACAGGCTGCTTACACATTTTATCTAGAGAGCTAGGCTATGCTAG 1140  
Db 8183 AGGAGAAAGGCTCACAGGCTGCTTACACATTTTATCTAGAGAGCTAGGCTATGCTAG 8242

Qy 1141 TCGTAGCTGGCAATTAACAACTGAAGCACTTCTAGTTCATGTGAGAGATGAATTTAAC 1200  
Db 8243 TCGTAGCTGGCAATTAACAACTGAAGCACTTCTAGTTCATGTGAGAGATGAATTTAAC 8302  
Qy 1201 ATATCTCAACCCCTCTGCACTGAAGCAAGACTAAGTACTCAAGTACCACTTATCTGTC 1260  
Db 8303 ATATCTCAACCCCTCTGCACTGAAGCAAGACTAAGTACTCAAGTACCACTTATCTGTC 8362  
Qy 1261 ACTTACTATATGAAGGCACTGTACTCAACATTTTACATGATTTATTAATTAATGAGCC 1320  
Db 8363 ACTTACTATATGAAGGCACTGTACTCAACATTTTACATGATTTATTAATTAATGAGCC 8422  
Qy 1321 CCAACTCTATGAGAACTGAAGGTTAGAGAGTATCTCATTCATTTATTAACAAGTGG 1380  
Db 8423 CCAACTCTATGAGAACTGAAGGTTAGAGAGTATCTCATTCATTTATTAACAAGTGG 8482  
Qy 1381 CAACCTGAGTCTGAACCTGAGTCTATCCAACTGCAAGACCTGAGTCCCAATGCTACA 1440  
Db 8483 CAACCTGAGTCTGAACCTGAGTCTATCCAACTGCAAGACCTGAGTCCCAATGCTACA 8542  
Qy 1441 CAATTCATATCAAGTAAAGGAAAGATTTGATTTGCTCAGAACTGATAGGGCA 1500  
Db 8543 CAATTCATATCAAGTAAAGGAAAGATTTGATTTGCTCAGAACTGATAGGGCA 8602  
Qy 1501 TATGTTCAATTAATTAACATTAACAAAGATTTATGTTGAAATTAATTAATTAACAACA 1560  
Db 8603 TATGTTCAATTAATTAACATTAACAAAGATTTATGTTGAAATTAATTAATTAACAACA 8662  
Qy 1561 TAAACCTTATTAACCTGATCTAATTAATGCTCCGCAACAAGATCTGTAATCTCTCA 1620  
Db 8663 TAAACCTTATTAACCTGATCTAATTAATGCTCCGCAACAAGATCTGTAATCTCTCA 8722  
Qy 1621 GGGCATCTGTTGTGCTGCTGTTTCCCTTAATCTTATATGATGAGGCAATCTAATGCAAT 1680  
Db 8723 GGGCATCTGTTGTGCTGCTGTTTCCCTTAATCTTATATGATGAGGCAATCTAATGCAAT 8782  
Qy 1681 ATGTAAGGCCATTTTCTCTCAAGATGTAAGTATCTCTTATGAATTTGATGAATGCA 1740  
Db 8783 ATGTAAGGCCATTTTCTCTCAAGATGTAAGTATCTCTTATGAATTTGATGAATGCA 8842  
Qy 1741 TTAACCTTCAAGGCTACGAGTTCATTTATAGTCACTGAGGCAAGTAAATTAAGTCA 1800  
Db 8843 TTAACCTTCAAGGCTACGAGTTCATTTATAGTCACTGAGGCAAGTAAATTAAGTCA 8902  
Qy 1801 TGTCGAAAGTATGACCTTAATAAATTAATTAATGATGAACCACTGCACTCTTGGG 1860  
Db 8903 TGTCGAAAGTATGACCTTAATAAATTAATTAATGATGAACCACTGCACTCTTGGG 8962  
Qy 1861 GAAAAAGTATGAGTATTAATCTCTTATGAGAGTCTTATGCTTCCCAAAAGTATGAGAA 1920  
Db 8963 GAAAAAGTATGAGTATTAATCTCTTATGAGAGTCTTATGCTTCCCAAAAGTATGAGAA 9022  
Qy 1921 AATAAATCTGCTGAGGCTGGAACAAGCTCTGCTTCTGCTGCTATTTGTTAGT 1980  
Db 9023 AATAAATCTGCTGAGGCTGGAACAAGCTCTGCTTCTGCTGCTATTTGTTAGT 9082  
Qy 1981 TTTTATATGTTCAATTTATGAACTTGTGAGCTCCAAAGTAAAGTGAAGTTGATC 2040  
Db 9083 TTTTATATGTTCAATTTATGAACTTGTGAGCTCCAAAGTAAAGTGAAGTTGATC 9142  
Qy 2041 CTTACAGAGGCACTTCAATTTATGAGAAACAAAAGCCCAATCTCTGCTCCAGACCTTA 2100  
Db 9143 CTTACAGAGGCACTTCAATTTATGAGAAACAAAAGCCCAATCTCTGCTCCAGACCTTA 9202  
Qy 2101 CCCCAAATCCCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2160  
Db 9203 CCCCAAATCCCTGCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 9262  
Qy 2161 TAGAGGTGCAAGTATCTAGAAAGTGAAGAAATGAGTATGACATTAAGTGAAGAGAGA 2220  
Db 9263 TAGAGGTGCAAGTATCTAGAAAGTGAAGAAATGAGTATGACATTAAGTGAAGAGAGA 9322

```

QY 2221 AAAATGGGACCCTTCATGATGTTCTTCCCTTCGTGTTCACAATGCTCCGATA 2280
Db 9323 AAAATGGGACCCTTCATGATGTTCTTCCCTTCGTGTTCACAATGCTCCGATA 9382
QY 2281 TAATTTTACAGAGGTATATACATTTTCTTTTACACCTGGAAGGCTGGAGAAA 2340
Db 9383 TAATTTTACAGAGGTATATACATTTTCTTTTACACCTGGAAGGCTGGAGAAA 9442
QY 2341 CTTTGTACCATCATATAAATTCATCTTCAAGTCATTCATGTTATTTCAAGATCA 2400
Db 9443 CTTTGTACCATCATATAAATTCATCTTCAAGTCATTCATGTTATTTCAAGATCA 9502
QY 2401 AATAGCTGACAAATATCTTTTGTATTAACATGAAAGAAACACATCCTCTGACCAATAT 2460
Db 9503 AATAGCTGACAAATATCTCTTTGTATTAACATGAAAGAAACACATCCTCTGACCAATAT 9562
QY 2461 TAATTCGCACTTTAGATATAGAAATTAATTAATCTAGTCATTTGAATGAAATCTGAATCA 2520
Db 9563 TAATTCGCACTTTAGATATAGAAATTAATTAATCTAGTCATTTGAATGAAATCTGAATCA 9622
QY 2521 TTTTCATATGATATAAAGATATTTATTTAAAGTAATTCATGAGCAATTTATATTAAG 2580
Db 9623 TTTTCATATGATATAAAGATATTTATTTAAAGTAATTCATGAGCAATTTATATTAAG 9682
QY 2581 TAGGATTTTCAATATGTTTAAAGATTTATTCAGGAAACAAAGTTTCTCAAAATTTATAGCA 2640
Db 9683 TAGGATTTTCAATATGTTTAAAGATTTATTCAGGAAACAAAGTTTCTCAAAATTTATAGCA 9742
QY 2641 GAAAAATTTTATCTAGATACAGTCTTTTCATTTAAGTCTCTGTAATTAATCTGTAAT 2700
Db 9743 GAAAAATTTTATCTAGATACAGTCTTTTCATTTAAGTCTCTGTAATTAATCTGTAAT 9802
QY 2701 TTCTAATTTATACAAGACTAAATTAATTTATATTAACAAATTAATTTATTTTACTTCAA 2760
Db 9803 TTCTAATTTATACAAGACTAAATTAATTTATATTAACAAATTAATTTATTTTACTTCAA 9862
QY 2761 ATGCTTAATTAATAGTATATAAATCATTTTATTTCTGAGGAAAGACATATCAACTTTT 2820
Db 9863 ATGCTTAATTAATAGTATATAAATCATTTTATTTCTGAGGAAAGACATATCAACTTTT 9922
QY 2821 TAAAGTATGAAGTAAATTAAGATTTTATCTTAATTTATTTTAAAGTTTCAAT 2880
Db 9923 TAAAGTATGAAGTAAATTAAGATTTTATCTTAATTTATTTTAAAGTTTCAAT 9982
QY 2881 ATAAAGATGAATAGATCTAAGTATATGTTATTTAATTAAGTTTAAATTTTTCGC 2940
Db 9983 ATAAAGATGAATAGATCTAAGTATATGTTATTTAATTAAGTTTAAATTTTTCGC 10042
QY 2941 ATGTCATATACAGCTTTATTTATTCATGATTTATTCCTTTTAAAGATGTCAAATGAA 3000
Db 10043 ATGTCATATACAGCTTTATTTATTCATGATTTATTCCTTTTAAAGATGTCAAATGAA 10102
QY 3001 TCAGCTCACTTCGATCTGTAACAAATACATGTTTGTGATCTTGACACAGAGGTTTTA 3060
Db 10103 TCAGCTCACTTCGATCTGTAACAAATACATGTTTGTGATCTTGACACAGAGGTTTTA 10162
QY 3061 ACCCTGACAGCGAGATTCATGTTGAGCAAGAGCCATCAAGATCCCGACGACACTTG 3120
Db 10163 ACCCTGACAGCGAGATTCATGTTGAGCAAGAGCCATCAAGATCCCGACGACACTTG 10222
QY 3121 TCTCATCAAGGTTGGAATATTAAGGCACTTGGATATACAGTATTAAGATTTCACTGATG 3180
Db 10223 TCTCATCAAGGTTGGAATATTAAGGCACTTGGATATACAGTATTAAGATTTCACTGATG 10282
QY 3181 TGGCAATGTTCTCTGACACTGGGACGACATTAACGTTTGGCTTGGGTTATCTCAAAAGC 3240
Db 10283 TGGCAATGTTCTCTGACACTGGGACGACATTAACGTTTGGCTTGGGTTATCTCAAAAGC 10342
QY 3241 AAAAGAAAGTAAAGAAAGAAAGTAAAGAAAGGAAAGAAAGTTGATTTGATTTTAAAGC 3300
Db 10343 AAAAGAAAGTAAAGAAAGAAAGTAAAGAAAGGAAAGAAAGTTGATTTGATTTTAAAGC 10402
QY 3301 ATGCAAAAACCTGCAAAATCTCTGTTATATTAATTAATTAATGCTGATGTTGCTGGCCA 3360

```

```

Db 10403 ATGCAAAAACCTGCAAAATCTCTGTTATATTAATTAATGCTGATGTTGCTGGCCA 10462
QY 3361 GTGATCTGATGATGAAGACAGCGACGACGAG 3390
Db 10463 GTGATCTGATGATGAAGACAGCGACGACGAG 10492

RESULT 2
BD233527
LOCUS BD233527 10492 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel promoter sequence of myostatin gene.
ACCESSION BD233527
VERSION BD233527.1 GI:33043297
KEYWORDS JP 2002519059-A/1.
SOURCE
ORGANISM
Bos sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 10492)
AUTHORS Bass,J.J., Jeanplong,F., Kambadur,R. and Sharma,M.
TITLE Novel promoter sequence of myostatin gene
JOURNAL Patent: JP 2002519059-A 1 02-JUL-2002;
AGRESEARCH LTD
OS Bos sp. (bovine)
PN JP 2002519059-A/1
PD 02-JUL-2002
PP 07-JUL-1999 JP 2000558200
PR 07-JUL-1998 NZ 330902
PI JAMES J BASS, FERENC JEANPLONG, RAVI KAMBADUR, MRIDULA SHARMA PC
C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/10, C12N5/
00
CC Novel promoter sequence of myostatin gene
FH Key Location/Qualifiers
FT promoter (1)..(10402)
FT enhancer (6728)..(6734)
FT enhancer (7874)..(7880)
FT misc_signal (9819)..(9832)
FT TATA_signal (9457)..(9463)
FT enhancer (9860)..(9866)
FT enhancer (10095)..(10101)
FT CAAT_signal (10197)..(10202)
FT TATA_signal (10240)..(10247)
FT TATA_signal (10264)..(10271)
FT CDS (10403)..(10492).

FEATURES
source
1..10492
/organism="Bos sp."
/mol_type="genomic DNA"
/db_xref="taxon:29061"

ORIGIN
Query Match 100.0%; Score 3390; DB 6; Length 10492;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTGCTCCGAAGCCATAGAGAGTTGCAATATCCCGCATGAGAGAGAAACACGTTCC 60
Db 7103 TGCCTGCTCCGAAGCCATAGAGAGTTGCAATATCCCGCATGAGAGAGAAACACGTTCC 7162
QY 61 TTGAATTTCTTGAGTACCTCTTAATTCATTCATGATGCTGACCTCCGAGATTGGATAGAG 120
Db 7163 TTGAATTTCTTGAGTACCTCTTAATTCATTCATGATGCTGACCTCCGAGATTGGATAGAG 7222
QY 121 CTGACTCTCATTTATTCACAGTGTATGTTCTAACCAATCACTGCAACATGAATTAAGTG 180
Db 7223 CTGACTCTCATTTATTCACAGTGTATGTTCTAACCAATCACTGCAACATGAATTAAGTG 7282
QY 181 ATTCTGGAACACGCCCCCTTAGGGGAACCTCAAGGTTAAGTTCCCTGACGCTTGCTCA 240
Db 7283 ATTCTGGAACACGCCCCCTTAGGGGAACCTCAAGGTTAAGTTCCCTGACGCTTGCTCA 7342

```

QY 241 CGTTTTGTTAACCATCAATTAATAACCTGTTTGTGTGATTCGTGTTTAAATAT 300  
DB 7343 CGTTTTGTTAACCATCAATTAATAACCTGTTTGTGTGATTCGTGTTTAAATAT 7402  
QY 301 CTTTATTTAATAGTACTGCTAATCTTCAACATTTGGTTCAACACAAAAGCCCTATT 360  
DB 7403 CTTTATTTAATAGTACTGCTAATCTTCAACATTTGGTTCAACACAAAAGCCCTATT 7462  
QY 361 AACTGGAAAGCCGTAATGAAGCTTACATTAACACATTTGTTTCTATGAGAAATTT 420  
DB 7463 AACTGGAAAGCCGTAATGAAGCTTACATTAACACATTTGTTTCTATGAGAAATTT 7522  
QY 421 TTCCTTCAGTCTGECACAGCCCTTCTGTTAAATTTGTGGAACAAATATATACATG 480  
DB 7523 TTCCTTCAGTCTGECACAGCCCTTCTGTTAAATTTGTGGAACAAATATATACATG 7582  
QY 481 AAATGACTATTTATTAAGTATTTTAACTGTACATGTGACATTTAGTACATTTAC 540  
DB 7583 AAATGACTATTTATTAAGTATTTTAACTGTACATGTGACATTTAGTACATTTAC 7642  
QY 541 CTGTGCTGGAACTATGATCAACATTCATCTGAAACTTTTGTATCTTCGAAATTGAA 600  
DB 7643 CTGTGCTGGAACTATGATCAACATTCATCTGAAACTTTTGTATCTTCGAAATTGAA 7702  
QY 601 AACTGTGACTATTTGACAGATGACTTCCCATCAACACGACACCTTCTCCAGCC 660  
DB 7703 AACTGTGACTATTTGACAGATGACTTCCCATCAACACGACACCTTCTCCAGCC 7762  
QY 661 CCGGACACACATCTCTTCTTCCATGACATGATCTCTGTGCTTGAAACACAGCCCTTCA 720  
DB 7763 CCGGACACACATCTCTTCTTCCATGACATGATCTCTGTGCTTGAAACACAGCCCTTCA 7822  
QY 721 ACACTAGCTTGGGGGGGCACTGTAAAGCAAGATCACTCCCTACCGGACCAATGTGAC 780  
DB 7823 ACACTAGCTTGGGGGGGCACTGTAAAGCAAGATCACTCCCTACCGGACCAATGTGAC 7882  
QY 781 ACAAAATATTAATAAGCATGTGGCATATGATTCGAAATAAGGATGCTGTGTAATGA 840  
DB 7883 ACAAAATATTAATAAGCATGTGGCATATGATTCGAAATAAGGATGCTGTGTAATGA 7942  
QY 841 GGGCTGAAACAGGACAGAAATTTGACTGATGCTCAAGTGGGATCTGTGTGTTGGA 900  
DB 7943 GGGCTGAAACAGGACAGAAATTTGACTGATGCTCAAGTGGGATCTGTGTGTTGGA 8002  
QY 901 AGCCTCAAAATTTTCCATTTGTTCTGTGATGACGCAAAATGCTTATTAAGACCTGTAGG 960  
DB 8003 AGCCTCAAAATTTTCCATTTGTTCTGTGATGACGCAAAATGCTTATTAAGACCTGTAGG 8062  
QY 961 ATTGATTATGAAGTTAAGATTAATCTGACAGACATTAATGTGCAAGACGGGATCCAT 1020  
DB 8063 ATTGATTATGAAGTTAAGATTAATCTGACAGACATTAATGTGCAAGACGGGATCCAT 8122  
QY 1021 GAATTAAGAGCACTGACCATGTGGAATGATTAATCTTTGTTTCTTTTATTCAGAGCTA 1080  
DB 8123 GAATTAAGAGCACTGACCATGTGGAATGATTAATCTTTGTTTCTTTTATTCAGAGCTA 8182  
QY 1081 AGAGAAAGGCTCAGAGGGCTGACCTTAACACATTTTACTAGAGAGCTAGCCTATGTCAG 1140  
DB 8183 AGAGAAAGGCTCAGAGGGCTGACCTTAACACATTTTACTAGAGAGCTAGCCTATGTCAG 8242  
QY 1141 TCGGTAGCTGGCAATTAACAACTGAAGCATTTCTAGTTCAATGTGAGAGATGAATTTAAC 1200  
DB 8243 TCGGTAGCTGGCAATTAACAACTGAAGCATTTCTAGTTCAATGTGAGAGATGAATTTAAC 8302  
QY 1201 ATATATCTCAACCCCTCTGCTATGAAACAGAGACTTAAGTACAGTACCATATCAATC 1260  
DB 8303 ATATATCTCAACCCCTCTGCTATGAAACAGAGACTTAAGTACAGTACCATATCAATC 8362  
QY 1261 ACTTAATATGACAGGCACTGTAATCAACAAATTTACATGATTAATGAATTAACATGCC 1320  
DB 8363 ACTTAATATGACAGGCACTGTAATCAACAAATTTACATGATTAATGAATTAACATGCC 8422  
QY 1321 CCAACTCTATGAGAAAGCTGAAGGTTAGAAAGTATCTCATTTATTTACAGATGG 1380

DB 8423 CCAACTCTATGAGAAAGCTGAAGGTTAGAAAGTATCTCATTTATTTACAGATGG 8482  
QY 1381 CCAACTGAGATCTGAATCTGAGCTATCCAACTCCAGGACCTGAGATCCCAATTTGCTACA 1440  
DB 8483 CCAACTGAGATCTGAATCTGAGCTATCCAACTCCAGGACCTGAGATCCCAATTTGCTACA 8542  
QY 1441 CAATTCATCAAGTTTAAAGGAAAGGATTTGATTTGCTCAGAAAGTATAGGGGCA 1500  
DB 8543 CAATTCATCAAGTTTAAAGGAAAGGATTTGATTTGCTCAGAAAGTATAGGGGCA 8602  
QY 1501 TATGTTTCAATTTATACATTTACAAAGATTTATATGTTGAAATAATTTATCAACAAA 1560  
DB 8603 TATGTTTCAATTTATACATTTACAAAGATTTATATGTTGAAATAATTTATCAACAAA 8662  
QY 1561 TAAACCTTTAAGCCGATCTAATATCTGCTCCGCAACAAAGACTATCTGAAATCTTTCA 1620  
DB 8663 TAAACCTTTAAGCCGATCTAATATCTGCTCCGCAACAAAGACTATCTGAAATCTTTCA 8722  
QY 1621 GGGCATCTGATTTGTGCTGCTGTTTCTTAAATCTTAAATGATGGCAATCTAATGCAAT 1680  
DB 8723 GGGCATCTGATTTGTGCTGCTGTTTCTTAAATCTTAAATGATGGCAATCTAATGCAAT 8782  
QY 1681 ATGTAAAGGCAATTTTCTCAAGAGATGATACCTCTTAAAGATTTGATGAATAATGCA 1740  
DB 8783 ATGTAAAGGCAATTTTCTCAAGAGATGATACCTCTTAAAGATTTGATGAATAATGCA 8842  
QY 1741 TTAACTTTTCAAGGCTACGATGATGATTTAGTACATGAGGAGTAAATTAAGTACAA 1800  
DB 8843 TTAACTTTTCAAGGCTACGATGATGATTTAGTACATGAGGAGTAAATTAAGTACAA 8902  
QY 1801 TGTGCGAAAGTATGACCTTAAATAATTTATGATGAACCACTGCACTCTTGTGG 1860  
DB 8903 TGTGCGAAAGTATGACCTTAAATAATTTATGATGAACCACTGCACTCTTGTGG 8962  
QY 1861 GAAAAAGTATGATTAATCTCTTATGAGAGTCTTATGCTTCCCAAAAGTATGAGAAA 1920  
DB 8963 GAAAAAGTATGATTAATCTCTTATGAGAGTCTTATGCTTCCCAAAAGTATGAGAAA 9022  
QY 1921 AATTAATCTCTGAGGCTGAGAAACAGCTTCTGTTTCTGCTGCTAATTTGTTAGGT 1980  
DB 9023 AATTAATCTCTGAGGCTGAGAAACAGCTTCTGTTTCTGCTGCTAATTTGTTAGGT 9082  
QY 1981 TTTTAAATAGTTCATTTGATTAAGACCTTGTGCTCCCAAGCTAAGTGTGATGATC 2040  
DB 9083 TTTTAAATAGTTCATTTGATTAAGACCTTGTGCTCCCAAGCTAAGTGTGATGATC 9142  
QY 2041 CTTACAGAGGCACTTCAATTTTACAGAAACAAAAGCCCATTTCTGTGCTCCAGACCTTA 2100  
DB 9143 CTTACAGAGGCACTTCAATTTTACAGAAACAAAAGCCCATTTCTGTGCTCCAGACCTTA 9202  
QY 2101 CCCCAAATCCCTGACAGGTGCTGCTCCGCTCAATGAGAAATGAGCAAGGAAATGAC 2160  
DB 9203 CCCCAAATCCCTGACAGGTGCTGCTCCGCTCAATGAGAAATGAGCAAGGAAATGAC 9262  
QY 2161 TAGAGGTGCAACGTACTAGAAAGTAAAGAAATGACCTAGCACTACTAGAAAGCAGA 2220  
DB 9263 TAGAGGTGCAACGTACTAGAAAGTAAAGAAATGACCTAGCACTACTAGAAAGCAGA 9322  
QY 2221 AAAATGGGCAACCTTCAATGATGTGTTCTTTTCCCTTTCTGTGTTCACATGCTCCGATA 2280  
DB 9323 AAAATGGGCAACCTTCAATGATGTGTTCTTTTCCCTTTCTGTGTTCACATGCTCCGATA 9382  
QY 2281 TAAATTTACAGAGGTAATTAATCAATTTTCTTTTCAACACTGAAAGGCTGAGAAA 2340  
DB 9383 TAAATTTACAGAGGTAATTAATCAATTTTCTTTTCAACACTGAAAGGCTGAGAAA 9442  
QY 2341 CTTTGTATACCATCAATAAATTCATATCTTCTAAGTCAATCTATGTTATTTCTAAGTCA 2400  
DB 9443 CTTTGTATACCATCAATAAATTCATATCTTCTAAGTCAATCTATGTTATTTCTAAGTCA 9502  
QY 2401 AATGCTGACATATCTCTTTGTAATTAACATGAAAGAAACACATCTCTGAGCAATAT 2460







|    |        |                                                                 |          |
|----|--------|-----------------------------------------------------------------|----------|
| Oy | 1741   | TTAACTTTTCAGGCGTACAGATGTGACTTTTAGTGCCTGAGGCGATGAATTAATGTACAA    | 1800     |
| Dp | 103761 | TTAACTTTTCAGGCGTACAGATGTGACTTTTAGTGCCTGAGGCGATGAATTAATGTACAA    | 10370202 |
| Oy | 1801   | TGTGCGAAGTAGTGACCTTAAAAATAATATTTGATATGAACCACTGCACTCTCTTGGG      | 1860     |
| Dp | 103701 | TGTGCGAAGTAGTGACCTTAAAAATAATATTTGATATGAACCACTGCACTCTCTTGGG      | 10346420 |
| Oy | 1861   | GAATAAAGTAAAGTAACTCTCTTAGAGAGTCTAGTCTCCCAAAAGTAACTAGAGAA        | 1920     |
| Dp | 103641 | GAATAAAGTAAAGTAACTCTCTTAGAGAGTCTAGTCTCCCAAAAGTAACTAGAGAA        | 1035822  |
| Oy | 1921   | AATAAATCTCCTGTGGCCCTGAGAAACAGCTTCTGTCTTCTGTGCTGATATTTTGTAGGT    | 1980     |
| Dp | 103581 | AATAAATCTCCTGTGGCCCTGAGAAACAGCTTCTGTCTTCTGTGCTGATATTTTGTAGGT    | 10352222 |
| Oy | 1961   | TTTTTAATAGTCAATTTGATTAAGCTTTGTGGCTCCCAAAAGTAAAGGTGAGTTGATC      | 2040     |
| Dp | 103521 | TTTTTAATAGTCAATTTGATTAAGCTTTGTGGCTCCCAAAAGTAAAGGTGAGTTGATC      | 10346282 |
| Oy | 2041   | CCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCCCAATCTCTGCTCCGACGCTTA      | 2100     |
| Dp | 103461 | CCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCCCAATCTCTGCTCCGACGCTTA      | 10340202 |
| Oy | 2101   | CCCCAAATCCCTGCCAGGTGTCTGCCCTCCGCTCAATAGAGAACTGGCAAGAAAGTAC      | 2160     |
| Dp | 103401 | CCCCAAATCCCTGCCAGGTGTCTGCCCTCCGCTCAATAGAGAACTGGCAAGAAAGTAC      | 10334242 |
| Oy | 2161   | TAGGAGGTGCGCACTATPACTAGAGAGTAAAGAAAAATGAGACTAGCACTATCTAGAAACAGA | 2220     |
| Dp | 103341 | TAGGAGGTGCGCACTATPACTAGAGAGTAAAGAAAAATGAGACTATCTAGAAACAGA       | 10328222 |
| Oy | 2221   | AAAAATGGGCAACCTTCATGATGATGTCTCTTCCCTTCTGTGTGATGACATGCTCCGATA    | 2280     |
| Dp | 103281 | AAAAATGGGCAACCTTCATGATGATGTCTCTTCCCTTCTGTGTGATGACATGCTCCGATA    | 10322222 |
| Oy | 2281   | TAAATTTACAGAGGGTAGATTAAGTCAATTTTTTCTTTACCACTGAGAGGCTGAGAGAAA    | 2340     |
| Dp | 103221 | TAAATTTACAGAGGGTAGATTAAGTCAATTTTTTCTTTACCACTGAGAGGCTGAGAGAAA    | 10316222 |
| Oy | 2341   | CTTTGTCCCATCATTAATAATTCACATCTCTTCAAGTCAATCTATGTTATTTCAAGATCA    | 2400     |
| Dp | 103161 | CTTTGTCCCATCATTAATAATTCACATCTCTTCAAGTCAATCTATGTTATTTCAAGATCA    | 10310202 |
| Oy | 2401   | AATAGCTGACATATCTCTTTGTATATAAACAATGAAAAACAATCCTCTGAGCAATAT       | 2460     |
| Dp | 103101 | AATAGCTGACATATCTCTTTGTATATAAACAATGAAAAACAATCCTCTGAGCAATAT       | 10304242 |
| Oy | 2461   | TAACTGCGAATTTAGAGTAGAGAGTAACTTAATCTAGTCAATTGAAACTGAAATACAA      | 2520     |
| Dp | 103041 | TAACTGCGAATTTAGAGTAGAGAGTAACTTAATCTAGTCAATTGAAACTGAAATACAA      | 10298282 |
| Oy | 2521   | TTTTCATATGAATTAAGAATATTAATTAAGAAATTCATGAGCAATTTAATTTAAG         | 2580     |
| Dp | 102981 | TTTTCATATGAATTAAGAATATTAATTAAGAAATTCATGAGCAATTTAATTTAAG         | 10292222 |
| Oy | 2581   | TAGATTTTCAATTAATGTGTTAAGAAATTTACAGGAGAAACAAGTTCTCAAAATTAAGCA    | 2640     |
| Dp | 102921 | TAGATTTTCAATTAATGTGTTAAGAAATTTACAGGAGAAACAAGTTCTCAAAATTAAGCA    | 10286282 |
| Oy | 2641   | GAATAATCTTTACTGTATCACAGTCTTTTCAATTAAGCTTCTGAAATTAATCTGAT        | 2700     |
| Dp | 102861 | GAATAATCTTTACTGTATCACAGTCTTTTCAATTAAGCTTCTGAAATTAATCTGAT        | 10280202 |
| Oy | 2701   | TTCTAATTATACAGACTTAAAAATAATTTATATTAACAATAAATAATTTTACTTCAA       | 2760     |
| Dp | 102801 | TTCTAATTATACAGACTTAAAAATAATTTATATTAACAATAAATAATTTTACTTCAA       | 10274242 |
| Oy | 2761   | ATGCTTAAGTAAATGTATGAATAATCAATTTATTTCTGAGGAGAAAGCATATCACTTT      | 2820     |
| Dp | 102741 | ATGCTTAAGTAAATGTATGAATAATCAATTTATTTCTGAGGAGAAAGCATATCACTTT      | 10268282 |

|            |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                |            |                 |
|------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------|------------|-----------------|
| QY         | 2821                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TAAGTATGAAGTGTAAATTTAAGATTTATTCACCTAAATTTAAATTTTAAAGTTTCAAT    | 2880       |                 |
| Db         | 102681                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TAAAGTATGAAGTGTAAATTTAAGATTTATTCACCTAAATTTAAATTTTAAAGTTTCAAT   | 10268      |                 |
| QY         | 2881                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ATAAAGATGATATGATCTAAGTGTATATGTATTTGTTAATAAAGTTTAAATTTTTCGC     | 2940       |                 |
| Db         | 102621                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATAAAGATGATATGATCTAAGTGTATATGTATTTGTTAATAAAGTTTAAATTTTTCGA     | 10252      |                 |
| QY         | 2941                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ATGTACATACAGCCTTTATTTATTCATATGATTTATTCCTTTTAAAGAGTATCAAATGA    | 3000       |                 |
| Db         | 102561                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATGTACATACAGCCTTTATTTATTCATATGATTTATTCCTTTTAAAGAGTATCAAATGA    | 10255      |                 |
| QY         | 3001                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCAGCTCACCCCTTGACTGTAACAAAATATCTGTTTGTGACTTGTACAGACAGGGTTTGA   | 3060       |                 |
| Db         | 102501                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCAGCTCACCCCTTGACTGTAACAAAATATCTGTTTGTGACTTGTACAGACAGGGTTTGA   | 10244      |                 |
| QY         | 3061                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ACCTCTGACAGCAGATTCATTTGTGTGACAAAGACCATCAAGATCCCGACACACTTG      | 3120       |                 |
| Db         | 102441                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ACCTCTGACAGCAGATTCATTTGTGTGACAAAGACCATCAAGATCCCGACACACTTG      | 10233      |                 |
| QY         | 3121                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCTCATCAAAAGTTGAAATATTAATAAGCCACTTGGAAATACATATTAATAAGATTCCTGTG | 3180       |                 |
| Db         | 102381                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCTCATCAAAAGTTGAAATATTAATAAGCCACTTGGAAATACATATTAATAAGATTCCTGTG | 10233      |                 |
| QY         | 3181                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TGGCAAGTTGCTCTTCAGACTGGCCAGGCAATTAAGTTGGCTGGGCTTACTAAAGC       | 3240       |                 |
| Db         | 102321                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGGCAAGTTGCTCTTCAGACTGGCCAGGCAATTAAGTTGGCTGGGCTTACTAAAGC       | 10222      |                 |
| QY         | 3241                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AAAGAAAGATGTAAAGAAAGATGTAAAGAAAGCAAGGAAAGATGTATTTGATTTTAAAC    | 3300       |                 |
| Db         | 102261                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAAGAAAGATGTAAAGAAAGATGTAAAGAAAGCAAGGAAAGATGTATTTGATTTTAAAC    | 10222      |                 |
| QY         | 3301                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ATGCAAAAACCTGCAAAATCTCTGTTTATATTTTACCTATTTATGCTGATTTGCTGGCCCA  | 3360       |                 |
| Db         | 102201                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATGCAAAAACCTGCAAAATCTCTGTTTATATTTTACCTATTTATGCTGATTTGCTGGCCCA  | 10211      |                 |
| QY         | 3361                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | GTGATCTGAAATGAGAACACGAGACACAG                                  | 3390       |                 |
| Db         | 102141                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GTGATCTGAAATGAGAACACGAGACACAG                                  | 102112     |                 |
| RESULT 4   | AC141852/c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 233029 bp                                                      | DNA linear | HTG 12-APR-2003 |
| LOCUS      | AC141852                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                |            |                 |
| DEFINITION | Bos taurus clone RP42-269D20, WORKING DRAFT SEQUENCE, 4 ordered pieces.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                |            |                 |
| ACCESSION  | AC141852                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                |            |                 |
| VERSION    | AC141852.2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | GI:29824447                                                    |            |                 |
| KEYWORDS   | HTG, HTGS PHASE2, HTGS_DRAFT.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                |            |                 |
| SOURCE     | Bos taurus (cow)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                |            |                 |
| ORGANISM   | Bos taurus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                |            |                 |
| REFERENCE  | Eukaryotes: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                |            |                 |
| AUTHORS    | 1 (bases 1 to 233029)<br>Antoniellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Carlaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-I., Hu,P., Hulle,B., Idol,J.R., Karlins,B., Kwong,P., Latic,P., Lee-Lin,S.-Q., Legaesi,R., Maduro,Q.L., Maduro,V.B., Margulis,E.H., Mastello,C., Masketi,B., McDowell,J., Paglisigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddi-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Simon,C., Stenitrop,S., Thomas,J.W., Thomas,P.J., Teipouri,V., Vogt,J.L., Weherby,K.D., Wiggins,L., Young,A. and Green,R.D. |                                                                |            |                 |
| TITLE      | NISC Comparative Sequencing Initiative                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                                                |            |                 |
| JOURNAL    | Unpublished                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                |            |                 |
| REFERENCES | 2 (bases 1 to 233029)<br>Green,B.D.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                |            |                 |
| AUTHORS    | Direct Submission                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                |            |                 |
| JOURNAL    | Submitted (19-MAR-2003) NIH Intramural Sequencing Center, 8717                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |                                                                |            |                 |
| REFERENCE  | Grovesmont Circle, Gaithersburg, MD 20877, USA<br>3 (bases 1 to 233029)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                |            |                 |

AUTHORS  
TITLE  
JOURNAL

Green, E.D.  
Direct Submission  
Submitted (12-APR-2003) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gaithersburg, MD 20877, USA  
On Apr 12, 2003 this sequence version replaced gi:29124102.

## COMMENT

----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: nisc.zoo@hgrl.nih.gov  
----- Project Information  
Center project name: djg  
Center clone name: 269D20

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies; the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

## ----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 232253 bases at least Q40  
Consensus quality: 232568 bases at least Q30  
Consensus quality: 232684 bases at least Q20  
Insert size: 200000; agarose-fp  
Insert size: 232729; sum-of-contigs  
Quality coverage: 11.69x in Q20 bases; agarose-fp  
Quality coverage: 10.05x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and the accession number will be preserved.  
\*  
\* 1 64168: contig of 64168 bp in length  
\* 64169 64268: gap of unknown length  
\* 64269 213649: contig of 149381 bp in length  
\* 213650 213749: gap of unknown length  
\* 213750 217486: contig of 3737 bp in length  
\* 217487 217587: gap of unknown length  
\* 217587 233029: contig of 15443 bp in length.

## FEATURES

## Source

1. .233029  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
/clone="RP42-269D20"  
/clone\_1id="RP42"  
1. .107006  
/note="clone overlaps with GenBank Accession Number AC141853 clone RP42-374H3 (center project name djp)"  
1. .64168  
/note="assembly\_fragment  
clone\_end:SP6  
vector\_side:left"  
64269. .213649  
/note="assembly\_fragment"  
213750. .217486  
/note="assembly\_fragment"  
217587. .233029  
misc\_feature  
misc\_feature  
misc\_feature  
misc\_feature

## ORIGIN

/note="assembly\_fragment  
clone\_end:T7  
vector\_side:right"

Query Match 98.1%; Score 3327.2; DB 2; Length 233029;  
Best Local Similarity 99.4%; Pred. No. 0;  
Matches 3371; Conservative 0; Mismatches 13; Indels 6; Gaps 3;  
1 TGCTGCTCCGAAGCATAGGAAGTTGCAATCCCGGACACTGAGAGGAAGAAACACGTC 60  
20057 TCGTCTCCGAAGCATAGGAAGTTGCAATCCCGGACACTGAGAGGAAGAAACACGTC 19998  
61 TTGAATTTCTTGAATCCTCTTAAATCAATGCTGACCTCCGAGATGATAG 120  
19997 TTGAATTTCTTGAATCCTCTTAAATCAATGCTGACCTCCGAGATGATAG 19938  
Qy 121 CTGACTCTATTTATTCACAGTGTTATGTTCTACCAATCACTGCCAATGAATAGTG 180  
Db CTGACTCTATTTATTCACAGTGTTATGTTCTACCAATCACTGCCAATGAATAGTG 19878  
Qy 181 ATTCCTGAACCACTGCCCTAGAGGAACTCAAGAGTTAGATCCGTCAGCTGTGCA 240  
Db ATTCCTGAACCACTGCCCTAGAGGAACTCAAGAGTTAGATCCGTCAGCTGTGCA 19818  
Qy 241 CGTTTGTATTAACCAATCAATTAATTAATCTGTTTGTGTCATTTCTTTAAATAT 300  
Db CGTTTGTATTAACCAATCAATTAATTAATCTGTTTGTGTCATTTCTTTAAATAT 19758  
Qy 301 CTTTATTTAATAGTACTGCTAATTTCTTCAACATTTGTTGTCACACCAAGCCCTATT 360  
Db CTTTATTTAATAGTACTGCTAATTTCTTCAACATTTGTTGTCACACCAAGCCCTATT 19757  
Qy 361 AACTGAAGCCCTGAATGAAGCTTACATTAACACATTTGTTTCTTATGAGAAATTT 420  
Db AACTGAAGCCCTGAATGAAGCTTACATTAACACATTTGTTTCTTATGAGAAATTT 19703  
Qy 421 TTCCTTGAAGCTTCCGACAGCTTTCTGTTAAATTTGAGCAAAATATATACATACATG 480  
Db TTCCTTGAAGCTTCCGACAGCTTTCTGTTAAATTTGAGCAAAATATATACATACATG 19643  
Qy 481 AAATGACTATTTATTTAATCTGATTTTAACTGTACAGTTCCAGTGCATTAAGTACATTAC 540  
Db AAATGACTATTTATTTAATCTGATTTTAACTGTACAGTTCCAGTGCATTAAGTACATTAC 19583  
Qy 541 CTGCTGTGGAACATGATTAACATTCATCTCTGAGACTTTTGTGATCTTCGAAATGAA 600  
Db CTGCTGTGGAACATGATTAACATTCATCTCTGAGACTTTTGTGATCTTCGAAATGAA 19523  
Qy 601 AACTCTGATCTATTTGACAGTACCTTTCCCATCAACACGCAACCTTCCTCCAGCCCC 660  
Db AACTCTGATCTATTTGACAGTACCTTTCCCATCAACACGCAACCTTCCTCCAGCCCC 19463  
Qy 661 CCGGACACCATCTCTTTCTTCCATGACAGTCACTGTGTCTGAGAAACAGCCCTTCA 720  
Db CCGGACACCATCTCTTTCTTCCATGACAGTCACTGTGTCTGAGAAACAGCCCTTCA 19403  
Qy 721 ACACTAGCTTGGGGGACATGTAAGCAAGAGTCACTCCATACGCGCAACAAAGTAC 780  
Db ACACTAGCTTGGGGGACATGTAAGCAAGAGTCACTCCATACGCGCAACAAAGTAC 19343  
Qy 781 ACAAAATATTAAGCATGTTGCAATGATTTGCAAAAGAGTGTCTCTAATATGA 840  
Db ACAAAATATTAAGCATGTTGCAATGATTTGCAAAAGAGTGTCTCTAATATGA 19283  
Qy 841 GGGCTGAACAAAGCAGAGATTTGACTAGTTGACTCTGAGTGGATCTGTGTGGA 900  
Db GGGCTGAACAAAGCAGAGATTTGACTAGTTGACTCTGAGTGGATCTGTGTGGA 19223  
Qy 901 AGCTCAATTTTCATTTCTGTGTCATGCAACAAAGTCTTATTAAGACTGTAGG 960  
Db AGCTCAATTTTCATTTCTGTGTCATGCAACAAAGTCTTATTAAGACTGTAGG 19163

QY 961 ATTGATTATGAAAGTTAAGATTAATCTGACGAAGACATTAATGTGCAAGCAGGGATCAT 1020  
DB 19103 ATTGATTATGAAAGTTAAGATTAATCTGACGAAGACATTAATGTGCAAGCAGGGATCAT 19044  
QY 1021 GAATTAAGACACTGACCAATGTGAAATGATTAATCTTTGTTTCTTTATTCAGGCACTA 1080  
DB 19043 GAATTAAGACACTGACCAATGTGAAATGATTAATCTTTGTTTCTTTATTCAGGCACTA 18984  
QY 1081 AGGGAAGAGGCTCAGAGGCTGCTTAACACATTTTATCTAGAGAGCTGAGCTTAATGAC 1140  
DB 18983 AGGGAAGAGGCTCAGAGGCTGCTTAACACATTTTATCTAGAGAGCTGAGCTTAATGAC 18924  
QY 1141 TCGGTACCTGCAATTAACAACTGAGCAGTTCTAGTTCATGTGAGGATGAATTAACC 1200  
DB 18923 TCGGTACCTGCAATTAACAACTGAGCAGTTCTAGTTCATGTGAGGATGAATTAACC 18864  
QY 1201 ATTAATCTCAACCCCTCTGCAATGAACAGACTAAGTACTGACAGTACCAATTAACATC 1260  
DB 18863 ATTAATCTCAACCCCTCTGCAATGAACAGACTAAGTACTGACAGTACCAATTAACATC 18804  
QY 1261 ACTTACTATATGACAGGCACTGTACTGACAACTTTATCATGTATTAATGAATTAATGCC 1320  
DB 18803 ACTTACTATATGACAGGCACTGTACTGACAACTTTATCATGTATTAATGAATTAATGCC 18744  
QY 1321 CCAACACTATATGAGAGCTGAAGCTTAGAAGATATCTCATTCATTATTAACACAGTGG 1380  
DB 18743 CCAACACTATATGAGAGCTGAAGCTTAGAAGATATCTCATTCATTATTAACACAGTGG 18684  
QY 1381 CAAACTGAGATCTGAACTCAGTCTATCCAACTCCAGGACCTGAGATCCCAATTCATCA 1440  
DB 18683 CAAACTGAGATCTGAACTCAGTCTATCCAACTCCAGGACCTGAGATCCCAATTCATCA 18624  
QY 1441 CAATTCATTAATCAATTTAAAGGGAAGAAAGATTTGATTTGCTCAAGATGTATAGGGCA 1500  
DB 18623 CAATTCATTAATCAATTTAAAGGGAAGAAAGATTTGATTTGCTCAAGATGTATAGGGCA 18564  
QY 1501 TATGTTCAATTAATTAACATTAACAAGATTTATATGTTGAAGAAATTAATTTATCAACAA 1560  
DB 18563 TATGTTCAATTAATTAACATTAACAAGATTTATATGTTGAAGAAATTAATTTATCAACAA 18504  
QY 1561 TAAATCTTTATTAAGCTGATCTAAATCTGCTGCGCAACAAAGACTATCTGAAATCTTCA 1620  
DB 18503 TAAATCTTTATTAAGCTGATCTAAATCTGCTGCGCAACAAAGACTATCTGAAATCTTCA 18444  
QY 1621 GGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
DB 18443 GGGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18384  
QY 1681 ATGTAAGGCAATTTTCTCAAGAGATGATACCTCTTAAGAAATTTGATGAATATGCA 1740  
DB 18383 ATGTAAGGCAATTTTCTCAAGAGATGATACCTCTTAAGAAATTTGATGAATATGCA 18324  
QY 1741 TTAATCTTTCAAGGCTAGTTCATTTATGTGCACTGAGGCAATTAATTAATGTGCA 1800  
DB 18323 TTAATCTTTCAAGGCTAGTTCATTTATGTGCACTGAGGCAATTAATTAATGTGCA 18264  
QY 1801 TGTGCGGAAGATGAGCACTTAATAATTTTGAATATGAAACCACTGCACTCTCTTGGG 1860  
DB 18263 TGTGCGGAAGATGAGCACTTAATAATTTTGAATATGAAACCACTGCACTCTCTTGGG 18204  
QY 1861 GAAAAAAGTAATGATTAACCTCTTGAAGATCTTGAAGCTTCCCAAAAGATGAGGAA 1920  
DB 18203 GAAAAAAGTAATGATTAACCTCTTGAAGATCTTGAAGCTTCCCAAAAGATGAGGAA 18144  
QY 1921 AATAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
DB 18143 AATAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 18084  
QY 1981 TTTTAAATAGTTCAATTTGATTTGACCTTGTGCTCCCAAGTAAAGTTGAGTTGATC 2040  
DB 18083 TTTTAAATAGTTCAATTTGATTTGACCTTGTGCTCCCAAGTAAAGTTGAGTTGATC 18024  
QY 2041 CCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCCCATTTCTGTGCTCCAGACCTTA 2100

DB 18023 CCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCCCATTTCTGTGCTCCAGACCTTA 17964  
QY 2101 CCCCNAATCCCTGCAAGTGTCTGCTCCCTCCGCTTAATATGAAATCTGCAAGAAATGAC 2160  
DB 17963 CCCCNAATCCCTGCAAGTGTCTGCTCCCTCCGCTTAATATGAAATCTGCAAGAAATGAC 17904  
QY 2161 TAGAGGTGCGCAGCTATGAGAAATGAGAAATGAGCTGAGCACTACTGAGAGGAGA 2220  
DB 17903 TAGAGGTGCGCAGCTATGAGAAATGAGAAATGAGCTGAGCACTACTGAGAGGAGA 17844  
QY 2221 AAAATGGCAACCTTCAATGATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2280  
DB 17843 AAAATGGCAACCTTCAATGATGATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 17784  
QY 2281 TAATTTACAGAGGTATGATATCAATTTTCTTTTCACTGAGAAAGCTGAGGAA 2340  
DB 17783 TAATTTACAGAGGTATGATATCAATTTTCTTTTCACTGAGAAAGCTGAGGAA 17724  
QY 2341 CTTGTTACCATCATTAATAATTCATATCTTAAGTCAATTTCTAATGATCA 2400  
DB 17723 CTTGTTACCATCATTAATAATTCATATCTTAAGTCAATTTCTAATGATCA 17664  
QY 2401 AATAGCTGACAAATCTCTTGTATTAATCAATGAAGAAACATATCCTGAGCAATAT 2460  
DB 17663 AATAGCTGACAAATCTCTTGTATTAATCAATGAAGAAACATATCCTGAGCAATAT 17604  
QY 2461 TAATTCGAACCTTTAGATAGAGTAAGTAATTAATCTATGATCAATGAAATGAAATCA 2520  
DB 17603 TAATTCGAACCTTTAGATAGAGTAAGTAATTAATCTATGATCAATGAAATGAAATCA 17544  
QY 2521 TTTTCATATGAATTAAGATATTAATTAAGATTAATCAATGAGCAATTAATTAAG 2580  
DB 17543 TTTTCATATGAATTAAGATATTAATTAAGATTAATCAATGAGCAATTAATTAAG 17484  
QY 2581 TAGATTTTCAATTAATGATTAAGATTAATTAATGAGGAAACAGTTCTCAATTAATGCA 2640  
DB 17483 TAGATTTTCAATTAATGATTAAGATTAATTAATGAGGAAACAGTTCTCAATTAATGCA 17424  
QY 2641 GAAATCTTTTATCTATGATCAAGCTCTTTCAATTAATGCTGCTGAAATTAATCTGAT 2700  
DB 17423 GAAATCTTTTATCTATGATCAAGCTCTTTCAATTAATGCTGCTGAAATTAATCTGAT 17364  
QY 2701 TTTCAATTAATCAAGCTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2760  
DB 17363 TTTCAATTAATCAAGCTTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17304  
QY 2761 ATGCTTACTTAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2820  
DB 17303 ATGCTTACTTAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17244  
QY 2821 TAAGTATGAAGGTAAATTAAGATTTATCACTTAATTAATTAATTAATTAATTAAT 2880  
DB 17243 TAAGTATGAAGGTAAATTAAGATTTATCACTTAATTAATTAATTAATTAATTAATTAAT 17184  
QY 2881 ATTAAGATGAATGAATCTAAGTATATGATTAATTAATTAATTAATTAATTAATTAAT 2940  
DB 17183 ATTAAGATGAATGAATCTAAGTATATGATTAATTAATTAATTAATTAATTAATTAAT 17124  
QY 2941 ATGTCATACAGGCTTTATTAATCATAGATTAATTAATTAATTAATTAATTAATTAAT 3000  
DB 17123 ATGTCATACAGGCTTTATTAATCATAGATTAATTAATTAATTAATTAATTAATTAATTAAT 17064  
QY 3001 TCACTCAACCTTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3060  
DB 17063 TCACTCAACCTTGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 17004  
QY 3061 ACCCTGACAGGCGATTAATGATGAGCAAGAGCAATGACAGATCCGACGACACTG 3120  
DB 17003 ACCCTGACAGGCGATTAATGATGAGCAAGAGCAATGACAGATCCGACGACACTG 16944  
QY 3121 TCTCATCAAGGTTGGAATTAATAAGCACTGGAATCAAGTATTAAGATTAATCACTGCTG 3180

|                        |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                   |                            |
|------------------------|--|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|----------------------------|
| Db                     |  | 16943                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TCTCATCAAGATTGGAAATVATAAAAACGACTTGGAAATPACAGTAATAAAGAATTTCACGTGCG | 16883                      |
| Oy                     |  | 3181                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | TGGCAAGTTGTTCTTCTCAGACTGGGCAGCCGAATTACGTTTTGGCTTGCTAACCAAACC      | 3240                       |
| Db                     |  | 16883                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TGGCAAGTTGTTCTTCTCAGACTGGGCAGCCGAATTACGTTTTGGCTTGCTTGCTAACCAAACC  | 16824                      |
| Oy                     |  | 3241                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AAAAAGAAAGATPAANAAGNAGATPAACAACAGGAAAGAAATGTGTATTAATTTTAAACC      | 3300                       |
| Db                     |  | 16823                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | AAAAAAAAAGTNAANAGAAAGATPAACAACAGGAAAGAAATGTGTATTAATTTTAAACC       | 16764                      |
| Oy                     |  | 3301                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ATGCCAAATCGCAAAATCTCTGTTTATATTTTAACTTATTTATGCTGATTTGTTGGCCCCA     | 3360                       |
| Db                     |  | 16763                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ATGCCAAATCGCAAAATCTCTGTTTATATTTTAACTTATTTATGCTGATTTGTTGGCCCCA     | 16704                      |
| Oy                     |  | 3361                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | GTCGATCTGGAATGAGAAACAGCACAGACAAG                                  | 3390                       |
| Db                     |  | 16703                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | GTGATCTCTGAATGAGAAACAGCACAGACAAG                                  | 16764                      |
| RESULT 5<br>ACI40968/c |  |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                   |                            |
| LOCUS                  |  | ACI40968                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 179158 bp                                                         | DNA linear HTG 03-APR-2003 |
| DEFINITION             |  | Sus scrofa clone RP44-467M16,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | WORKING DRAFT SEQUENCE,                                           | 3 ordered pieces.          |
| ACCESSION              |  | ACI40968                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                   |                            |
| VERSION                |  | ACI40968.2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | GI:29501861                                                       |                            |
| KEYWORDS               |  | HTG; HTS_PHASE2;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | HTS_DRAFT.                                                        |                            |
| SOURCE                 |  | Sus scrofa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | (pig)                                                             |                            |
| ORGANISM               |  | Sus scrofa                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                   |                            |
| REFERENCE              |  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;<br>Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.<br>1 (bases 1 to 179158)<br>Antker,N., Antocelli,A., Ayele,K., Beckstrom-Sternberg,S.M.,<br>Benjamin,B., Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,<br>Carriaga,K., Coleman,B., Engle,J.T., Granite,S.S., Guan,X., Gupta,J.,<br>Haghighi,P., Han,T., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,<br>Laric,P., Lee-Lin,S.-O., Legaspi,R., Maduro,Q.L., Maduro,V.B.,<br>Maguire,E.H., Masiello,C., Maekari,B., McDowell,J.,<br>Paguitigan,C., Pearson,R., Portroy,M.E., Prasad,A.,<br>Reddi-Dugue,N., Schandler,K., Schneider,M.G., Simon,C.,<br>Scantirrup,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,<br>Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.<br>NIHC Comparative Sequencing Initiative<br>Unpublished<br>2 (bases 1 to 179158)<br>Green,E.D.<br>Direct Submission<br>Submitted (06-MAR-2003) NIH Intramural Sequencing Center, 8717<br>Grovemont Circle, Gaithersburg, MD 20877, USA<br>3 (bases 1 to 179158)<br>Green,E.D.<br>Direct Submission<br>Submitted (03-APR-2003) NIH Intramural Sequencing Center, 8717<br>Grovemont Circle, Gaithersburg, MD 20877, USA<br>On Apr 3, 2003 this sequence version replaced gi:28867000. |                                                                   |                            |
| JOURNAL TITLE          |  | NISC Genome Center                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                   |                            |
| REFERENCE AUTHORS      |  | Center: NIH Intramural Sequencing Center<br>Center code: NISC<br>Web site: http://www.nihsc.nih.gov<br>Contact: nihsc.zoo@nihgri.nih.gov<br>----- Project Information<br>Center project name: dlyq<br>Center clone name: 467M16                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                   |                            |
| JOURNAL COMMENT        |  | The sequence data in this record represents an ‘enhanced’ version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and had been reviewed to rule out                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                   |                            |

```

gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.

----- Summary Statistics -----
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap, version 0.990139
Consensus quality: 178695 bases at least Q40
Consensus quality: 178865 bases at least Q30
Consensus quality: 178931 bases at least Q20
Insert size: 196000; agarose-fp
Insert size: 178958; sum-of-contigs
Quality coverage: 13.06x in Q20 bases; agarose-fp
Quality coverage: 14.30x in Q20 bases; sum-of-contigs

-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
  1 93877: contig of 93877 bp in length
  * 93878 93977: gap of unknown length
  * 93978 105317: contig of 11340 bp in length
  * 105318 105417: gap of unknown length
  * 105418 179158: contig of 73741 bp in length.
  Location/Qualifiers
    source
      1..179158
        /organism="Sus scrofa"
        /mol_type="genomic DNA"
        /db_xref="taxon:9823"
        /clone="RP4-467M16"
        /clone_1b="RP44"
        1..93877
          /note="assembly_fragment"
          clone_end:SP6
          vector_side:left"
          93978_..105317
            /note="assembly_fragment"
            105418..179158
              /note="assembly_fragment"
              clone_end:T7
              vector_side:right"

ORIGIN

Query Match 55.8%; Score 1890.8; DB 2; Length 179158;
Best Local Similarity 79.1%; Prid. No. 0;
Matches 2740; Conservative 0; Mismatches 532; Indels 190; Gaps 34;

  1 TGCGTCTCCGAGCCATPAGAGGTGGCAATCCCGGCACTGGAGAGGAAACAAGCTTC 60
Db 65212 TCCTTCTCTGGGGCTTTGGAAATTTGACGTCACTGACCTGGAGAGGAAATTAAGTTC 65153
  61 TTGAATTTCTTGAGTACCTCTTAATTCATTCATGCTGACCT-----CCGAGATTGG 114
Db 65152 TCAAACTTGTAGTACCTATTAATCACTTCAATTCATGACCTTGAGCAAGTTAATTG 65093
  115 ATAGAGCTGACTCTCATTTATTCACAGTGTATGTTCTAACCAATCACTGCCAAC----- 169
Db 65092 ACTCAGTGTGATCTCATTTATTCATTCACAGTGTGTCTTCAAAATCACTGCCAACACTGA 65033
  170 ATGAATTAAGGATTTCTGAAACCACTGCCCTTAGGGGAACCTACAAGTTAGATTCCGCTCA 229
Db 65032 ATGAATTAAGGATCTGAGCACTGAGCACTGCTCTTAGGGGAAGATCAAGTTAGTTCCATATCA 64973
  230 GCCCTGCTGACGTTTTTTGTTAACCAATCAATTAATTAACCTGTTTGTGTCATTTCTG 289
Db 64972 GCCTCTGCTGACATTTTTCACCAACCAATCAATTAATTAACCTGTTTGTGTCATTTCTG 64913
  290 TTTTAAATTAATCTTTAATTAATTAATTAATTAATTAATTTCTTCAACATTTGGTTCACCAACCA 349

```



```
Db 64912 TTTTAAATA--TTTATTTATATATATTTATGATTTATTAACATGTATTCATAGGCA 64855
Qy 350 AAGGCCCTATTAACTGGAAGCCCTGAATGAAGCTTACATTAACACATTTGTTTCTATG 409
Db 64854 A-----CACACTATACCTCAAGCCTGAATTAATGCTTACATTAATACATATTTTCCATTA 64799
Qy 410 AGAAAAATTTTCTTCACTGCTGCTGCAACAGCCTTCTGCTTAAATTTGGAACAAATA 469
Db 64798 AGAAAAATTTTCTTCACTGCTGCTGCAACAGCCTTCTGCTTAAATTTGGAACAAATA 64739
Qy 470 TACATAACATGAACCTGACTATTTATTTACTGATTTTACTGATTTTACTGATTTTACTGATTT 529
Db 64738 TACATAACATGAACCTGACTATTTATTTACTGATTTTACTGATTTTACTGATTTTACTGATTT 64702
Qy 530 AGTACATCTTACCTGCTGCTGCAACATGATTAACATTCATCTCTAGAACCTTTTGTATCT 589
Db 64701 AATACATTTATTTATTTGCTGCTGCAACATGATTAACATTCATCTCTAGAACCTTTTGTATCT 64642
Qy 590 CTGCAATTTGAACCTGCTGCTGCAACATGATTAACATTCATCTCTAGAACCTTTTGTATCT 649
Db 64641 CCCAAATTTGAACCTGCTGCTGCAACATGATTAACATTCATCTCTAGAACCTTTTGTATCT 64582
Qy 650 CTTGCAAGCCCCCGGCAACCATCTTCTTTTCAATGACATCTCTGCTGCTAGAAC 709
Db 64581 CTTGCAAGCCCCCGGCAACCATCTTCTTTTCAATGACATCTCTGCTGCTAGAAC 64522
Qy 710 ACAGCCCTTCAACCTGCTGCTGCTGCAACATGATTAACATTCATCTCTAGAAC 769
Db 64521 ACAGCCCTTCAACCTGCTGCTGCTGCAACATGATTAACATTCATCTCTAGAAC 64475
Qy 770 ACCAATGCAACACAAATATATTAAGATGCTGCTGCAACATTCATCTCTAGAAC 829
Db 64474 --AAAAACAAGTAAAAATGAAAAACATGTAATGTAAGATTTGCAAGATTTGCAAGGCACTT 64417
Qy 830 GC-TAAGTATGAGGCTGGAACCAAGCAGAGAAATTTGACTAGTTGACTCTGCTGCTGCTGCT 888
Db 64416 GCTTAAATCTGAGAGCTGGAACCAAGCAGAGAAATTTGACTAGTTGACTCTGCTGCTGCTGCT 64357
Qy 889 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 948
Db 64356 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64305
Qy 949 AGCATGTAAGATTTGATTTATGAAGTTAAG-ATTAATCTCAGCAAG-ACATTAATGCTCA 1006
Db 64304 AGTGCATGATGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGAT 64245
Qy 1007 AGCAGGATTCATGATTAACGAGCACTGACATGCTGGAATTAATCTTTGCTT 1066
Db 64244 TACAGGATTCATGATTAACGAGCACTGACATGCTGGAATTAATCTTTGCTT 64186
Qy 1067 TATTCAGGATTCATGATTAACGAGCACTGACATGCTGGAATTAATCTTTGCTT 1099
Db 64185 TATTCAGGATTCATGATTAACGAGCACTGACATGCTGGAATTAATCTTTGCTT 64126
Qy 1100 -GCTGCTTACACCATTTTATGAGAGCTAGCTATGCTAGCTGCTGCTGCTGCTGCTGCTGCT 1158
Db 64125 ATTTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64066
Qy 1159 AAACTGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1218
Db 64065 AAACCTGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 64006
Qy 1219 GCATGAACAGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 1278
Db 64005 GCATGAACAGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 63946
Qy 1279 ACTGATCTCAACATTTATCATGATTTATTTGATTTATCATGCCCCCAACACTCTATGAGGAA 1338
Db 63945 ACTGATCTCAACATTTATCATGATTTATTTGATTTATCATGCCCCCAACACTCTATGAGGAA 63887
Qy 1339 GCTGAGGTTTATGAGATGATCTCATTCATTTATTAACAGTGGCAAACTGAGATCTGAACT 1398
Db 63887 GCTGAGGTTTATGAGATGATCTCATTCATTTATTAACAGTGGCAAACTGAGATCTGAACT 63827
Qy 1399 CAGGCTATCCCACTCAGAGACTGAGATCCCATTTGCTACACATTTCTAATCAAGTTAA 1458
Db 63826 CAGGCTATCCCACTCAGAGACTGAGATCCCATTTGCTACACATTTCTAATCAAGTTAA 63768
Qy 1459 AAGGAAAAAGATTTGATTTGCTGCAAGGATTAAGGGGCAATGTT--ACAATTA 1515
Db 63767 AA-----AAAAAAATCTGATTTTACTCAGAAAGGATTAAGGAGATGATTTATGATTA 63710
Qy 1516 ACATTTAAGAAATTTATGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1575
Db 63709 ATATTTAAGAAATTTATGTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 63653
Qy 1576 CTGATCTAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1635
Db 63552 CTGATCTAATACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63593
Qy 1636 GTCTGCTTCTTCTTAACTTTTAACTGATGAGGCAATTAATGATTAATGATTAATGATTAAT 1695
Db 63592 GTCTGCTTCTTCTTAACTTTTAACTGATGAGGCAATTAATGATTAATGATTAATGATTAAT 63534
Qy 1696 TTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1755
Db 63533 TTCTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 63474
Qy 1756 ACTGATGCTATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1815
Db 63473 ACTGATGCTATTTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63414
Qy 1816 ACCTAAAAATTAATTTATGATTAATGAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1868
Db 63413 ACCTAAAAATTAATTTATGATTAATGAAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63354
Qy 1869 TAAATGATTAATCTCTTAAAGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 1928
Db 63353 TAAATGATTAATCTCTTAAAGATCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 63294
Qy 1929 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1988
Db 63293 TCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63234
Qy 1989 GTTCATTTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2048
Db 63233 GTTCATTTGATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63174
Qy 2049 GGCATCTTCAATTTTAAAGAAACAAAGCCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2108
Db 63173 GGCATCTTCAATTTTAAAGAAACAAAGCCCATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63114
Qy 2109 CCTGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2168
Db 63113 CCTGCGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 63059
Qy 2169 CGCAGATTAAGAAAGTGAAGAAATGAGCTAGCACTAGCACTAGCACTAGCACTAGCACTAG 2228
Db 63058 -----CTAGCACTAGCACTAGCACTAGCACTAGCACTAGCACTAGCACTAGCACTAG 63028
Qy 2229 CACCTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2288
Db 63027 CACCTTCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62968
Qy 2289 AGAGGATTAATTAATTAATTTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2348
Db 62967 AGAGGATTAATTAATTAATTTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62909
Qy 2349 CCATTAATTAATTAATTAATTTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2401
Db 62908 TCAGTCAATTAATTAATTAATTTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62849
Qy 2402 ATAGCTGATATCTCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2461
Db 62848 ATAGCTGATATCTCTTCTTAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62789
```



Db 79153 AGGAATTAATTTCCCTAAGTCATAGCAACCTCTTTTAAATGTGTAATA 79212  
 Qy 470 TACATACATGAACCTGACTATTAATTAAGTATTTAACTGTAAGTTGAGGCAATTA 529  
 Db 79213 TACATTAAGC-----AGTTCAGTGTACAGTTGAGTGCATTA 79249  
 Qy 530 AGTACCTTAACCTTGTGTGGAAGTAATGATCAATTCATCTAGAACTTTTGTACTT 589  
 Db 79250 AATACATTTAATTTGTGTGCAATCATGATCATATTCATCTCCAGAACTTTTGAACCTT 79309  
 Qy 590 CTGGAATTTGAAAATCTGCACTCTATTTGCAAGTACGTTTCCCTCCACACCGACCTT 649  
 Db 79310 CCCAAATTTGAAAATTTGTATCTATTAAGAGTGTGTTCCCTCCACACCGACCTT 79369  
 Qy 650 CCTCAGAGCCCGGACACCATCCCTCTTCCATGACATGATCCCTGAGGAGAC 709  
 Db 79370 CTTCCAGACATTTGTTGTAACACCATTTCTCTTCAATCAGACCTTCTGTATGTAGGAGC 79429  
 Qy 710 ACAGCCCTTCAMACCTACGCTTGGGGGCACTGTAGGCAAGGATCACTCCCTACCGCC 769  
 Db 79430 ACAG-----CACTATGCTTTGGGACATTTTAAACAGCAATCATCCCTA----- 79476  
 Qy 770 ACCAATGCAACAAAAATATATAAGATGTGCGCATGATTTGCAAAAAGGTGCTT 829  
 Db 79477 --AAAAACAAAGTAAAAATGTGAAAAACATGTGTACTATACAGATTTGCAAAAGGGCACTT 79534  
 Qy 830 GC--TAAGTATGAGGCTGAAACAAAGGAGAGAAATTAAGTACGTAGCTGACCTGAGTGC 888  
 Db 79535 GCTTAATCTGAGAGCTGAAACAAAGGAGAGAAATTTGCTTTGACCTCAACTGGAGCC 79594  
 Qy 889 CTGTGTGTGGAAACCTCAAAATTTTCCATTGTTCTGTGCAATGCACAAAATGCTTAATA 948  
 Db 79595 CTGTGT-----CTTCAAAATTTTGTGCTTTTGTATCAGGCAATTAAGCATATCA 79646  
 Qy 949 AGCACTGAAGGATTTGATTAATGAAGTTAAG--ATAATCTGCAAG--ACATAATGTGCA 1006  
 Db 79647 AGTCCCATGAGTATTTGATTTGAGATTAAAAATTAATTTTCAAGCAAGTGAACAAATTTGCA 79706  
 Qy 1007 AGCAGGGATCCATGAATTAACAGAGCTGACATGTGGAATTAATCTTTGTTCTT 1066  
 Db 79707 TACAGGAAATTCATGAATTAAGAGCAATTAAGCTGTACGAAATGA--CAGCTTTGTTCTT 79765  
 Qy 1067 TATTCAGGAGTAAAGAGAAAGCGCTCACAG----- 1099  
 Db 79766 TACTCCAGGTACTAAGAAATAAGAGCTGAATGTGGCTGTGATAGGTTGCTTGAAT 79825  
 Qy 1100 -GCTGCTTACACATTTTACTAGAGAGCTAGCTATGTCTAGTGGTACGCAATTAAC 1158  
 Db 79826 ATTTCACTTGCTCAGAGGCTTAAAGAGCTAGCTATGTGAATGATTAATGGCAGCTAC 79885  
 Qy 1159 AAACTGAAGAGTCTAGTTGATGAGAGATGAATTAACCATTAATCAACCCCTCT 1218  
 Db 79886 AACCTGAAGAGTCTAGTTGATGAGAGATGAATTAACCATTAATCAACCCCTCT 79945  
 Qy 1219 GCATGAACAGAGACTAAGTACTAAGTACAGTTATCAGTCACTTACTATATGACAGGC 1278  
 Db 79946 GCATGAACAGAGCAAAACATTAAGTACTAAGTATCAATCACTTACTATATGACAGGC 80005  
 Qy 1279 ACTGTACTCAACAATTTACATGATTAATGAATTAATCATGCCCCCAACCTCTATGAGGA 1338  
 Db 80006 ACTGTACTCAACAATTTACATGATTAATGAATTAATCATGCCCCCAACCTCTATGAGGA 80064  
 Qy 1339 GCTAAGGTTAAGAAAGTATCTCATTTCACTTATTAACAGTGGCAAACTGAGATCTGAAT 1398  
 Db 80065 GAACTAAGTATCTCATTTCACTTATTAACCTGTATGAAGTGCAGAAATTTGAATCT 80124  
 Qy 1399 CAGGTCTATCCAACTGAGAGCTGAGATCCCAATTTGCTACAGCAATTTCAATCAAGTTAA 1458  
 Db 80125 CAGGTCTATCTGATCTCCAAAGCT--ATTCCCAAGCTTTGCAATTTCTATCAAGTTTA 80183  
 Qy 1459 AAGGAAAAAGATTTGATTTGCTCAGAAAGTATAGGGGCAATGTT--ACAATTA 1515  
 Db 80184 AA-AAAAAATATCTGATTTACTCAGAAAGTATAGGAGCAATGTTATGATTAATTA 80242

Qy 1516 ACATTACAAAGATTTATATGTTGAAAAATAAATTAATCAACAAATAAACTTATAGC 1575  
 Db 80243 AATATTACAAAGATTTATATGTTGAAAAATAAATTTACCA--AAAAAACCTTATATAGC 80299  
 Qy 1576 CTGATCTAATACGCTCCGCAACAAAGACTATCTGAAATCCTTCAAGGCACTGTGTTGT 1635  
 Db 80300 CTGATCTAATATGCTCCACAAACAAAGATTTCTGAATCCTTCAAGGCACTGTGTTGT 80359  
 Qy 1636 GTCTGTTTCCCTAATCTTAAATGAGGGAAATCTAATGCAATTAATGAGGCATTT 1695  
 Db 80360 GTCTGTTTCCCTAATCTTAAATGAGGAGAGAGCTAATGATTAATGAGGCA--TTT 80418  
 Qy 1696 TTCTCAAGAGTATGATACCTCTTAAGAAATTTGATGAAATGATTAATCTTCAAGCT 1755  
 Db 80419 TTCTCAAGAGTATGATACCTCTTAAGAAATTTGATGAAATGATTAATCTTCAAGCT 80478  
 Qy 1756 ACTGAGTTGATTTTAAAGTCACTGAGGAGTAAATTAAGTCAATGTGCAAAAGTATG 1815  
 Db 80479 ACTGAGTTGATTTTAAAGTCACTGAGGAGTAAATTAAGTCAATGTGCAAAAGTATG 80538  
 Qy 1816 ACCTAAAAATTAATTTGATATGAATGAACCACTGACCTCTTGG-----GGAAAAAGTAA 1871  
 Db 80539 ACCTAAAAATTAATTTGATATGAACCACTGACATTTCTTGAIAAAAAAAGAAAGTAA 80598  
 Qy 1872 TGAATTAATCTCTTAAGAGTCTTACCTTCCCAAAAGTATGAGAAATAAATCTCC 1931  
 Db 80599 TGAATTAATCTCTTAAGAGTCTTACCTTCCCAAAAGTATGAGAAATAAATCTCC 80658  
 Qy 1932 TGTGGCTCGAAACAGCTTCTGTTTCTTGTCTGAGCTATTTGTTTAAATGATT 1991  
 Db 80659 TGTGGCTCGAAACAGCTTCTGTTTCTTGTCTGAGCTATTTGTTTAAATGATT 80718  
 Qy 1992 CATTTGATTAACCTTGTGCTCCCAAGCTAAGGTTGAAGTTGATCCCTACAGAGGC 2051  
 Db 80719 CATTTGATTAACCTTGTGCTCCCAAGCTAAGGTTGAAGTTGATCCCTACAGAGGC 80778  
 Qy 2052 CACTTCAATTTAGAGAAACAAAAAGCCCATCTCTGCTCCCAAGCTTAAACCCCAAT--CC 2110  
 Db 80779 CACTTCAATTTAGAGAAACAAAAAGCTCATTTCTGCTCCCAAGCTTAAACCCCAAT--CC 80838  
 Qy 2111 CTGCAAGGTCTGCTCCCTCGGTCAATTAAGAACTGGCAAAAGAGTACTAGAGGTGC 2170  
 Db 80839 CTGCAAGGTCTGCTCCCTCGGTCAATTAAGAACTGGCAAAAGAGGTGC----- 80891  
 Qy 2171 CACAGTACTAGGAAGTAAAGAAATGAGCTAGCACTACTAGAGAGCAAGAAATGGGCA 2230  
 Db 80892 -----CTAGCAAGAAATGGGAAACAGAAATATGGGCA 80924  
 Qy 2231 CCTTCAATGATGTTCTTCCCTTCTGTGTTCAACATGCTCCGATATATTAATTAAG 2290  
 Db 80925 CCTTCAATGATGTTCTTCCCTTCTGTGTTCAACATGCTCCGATATATTAATTAAG 80984  
 Qy 2291 AGGATGAATTAACATTTTCTTTTCCACTGGAAGGCTGAGAAACCTTGTTAAC 2350  
 Db 80985 AGAATGAAT--ACTACATTTTACTTTCACACATGGAATCTGAGGCAACCTGATTAAC 81043  
 Qy 2351 CATCATAAATTTCACTATC-----TCTAAGTATCTTANG--TTATTTAAGTCAAT 2403  
 Db 81044 AGTCAATAAATTAATTAATCTTTTCAATTAAGTATTAATTTCAAGCTCAAT 81103  
 Qy 2404 AGTGAACAATTTCTTTTGAATTAACAAATGAAGAAACACATCTGAGCAATTAATTA 2463  
 Db 81104 AGTGAACAATTTCTTTTGAATTAACAAATGAAGAAACACATCTGAGCAATTAATTA 81163  
 Qy 2464 TCTGCAACTTTAGAGTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTT 2523  
 Db 81164 TCTGCAACTTTAGAGTAAAGAAATTAATTAATTAATTAATTAATTAATTAATTT 81212  
 Qy 2524 TCAATTAAGTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTA--AAGTA 2582  
 Db 81213 TCAATTAAGTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 81272

```

Qy 2583 GGATTTTCATTATGTTAGATTATTCAGGGAACAAGTTCTCAAAATTAATGACGA 2642
Db 81273 TGATTTTCATTATGTTAGATTATTCAGGGAACAAGTTCTCAAAATTAATGACGA 81332
Qy 2643 AAATCTTTACTAGATACAGCTCTTTTCATTAAATC-----TTCCTGAATTAATCTG 2696
Db 81333 ATATATTTTACTAGATACAGCTCTTTTCATTAAATC-----TTCCTGAATTAATCTG 81392
Qy 2697 TATTT-TCTAATTTATACAGCTAATAAATTTAATATTAATAAATTAATTTTAC 2755
Db 81393 TATTTCTGATTTACAGGACTAATAAATTTAATAACAGCAATTAATTTCTTTTTC 81452
Qy 2756 TTCAAATGCTTACTTAATTAATTAATTAATTAATTTTCTGAGGAAAA--GCATTC 2813
Db 81453 CTCAAATGCTTCTAATAATTAATTAATTAATTTTCTGAGGAAAAACATTTTC 81512
Qy 2814 AACTTTTAAATGATGAAGTGAATTAATTAATTAATTTTCTAATAATTAATTTTAAAT 2873
Db 81513 AACTTTTAAATGATGAAGTGAATTAATTAATTAATTTTCTAATAATTAATTTTAAAT 81568
Qy 2874 TTCAATTAATAAGATGAATTAATTAATTAATTTTCTAATAATTAATTTTAAAT 2930
Db 81569 TTCAATTAATAAGATGAATTAATTAATTAATTTTCTAATAATTAATTTTAAAT 81628
Qy 2931 AATTTTTCGATGTCATACATACAGCTTATTAATTAATTAATTTTCTTTTAAAGATA 2990
Db 81629 AATTTTTCGATGTCATACATACAGCTTATTAATTAATTAATTTTCTTTTAAAGATA 81688
Qy 2991 GTCAAATGAATCAGCTACCTTGAATTAATTAATTAATTTTCTTTGAGACTTGACAGA 3050
Db 81689 GTCAAATGAATCAGCTACCTTGAATTAATTAATTAATTTTCTTTGAGACTTGACAGA 81748
Qy 3051 CAGGATTTTAACTCTGACAGCGAATTCATTTGAGAGCAAGCAATCAATCAATCCG 3110
Db 81749 CAGGATTTTAACTCTGACAGCGAATTCATTTGAGAGCAAGCAATCAATCAATCCG 81808
Qy 3111 ACAGACCTTGTCTCATCAAGTTGGAATATTAATAAGCCATTTGGAATCAATTAAGA 3170
Db 81809 ACAGACCTTGTCTCATCAAGTTGGAATATTAATAAGCCATTTGGAATCAATTAAGA 81866
Qy 3171 TTCACTGTTGGAAGTTGTTCTCTGACAGCTGGGAGGCAATTAAGTTTGGCTTGGCGTT 3230
Db 81867 TTCACTGTTGGAAGTTGTTCTCTGACAGCTGGGAGGCAATTAAGTTTGGCTTGGCGTT 81926
Qy 3231 ACTCAAAAGCAAAAGAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 3290
Db 81927 ACTCAAAAGCAAAAGAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 81981
Qy 3291 TTTTAAACCATGCAAAATCTGCAATCTCTGTTTATTTTAACTTATTAATGCTGATTTGT 3350
Db 81982 TTTTAAACCATGCAAAATCTGCAATCTCTGTTTATTTTAACTTATTAATGCTGATTTGT 82041
Qy 3351 TGCTGGCCAGTGAATGGAAGCAAGGAGAGAG 3390
Db 82042 TGCTGGCCAGTGAATGGAAGCAAGGAGAGAG 82081

```

RESULT 7  
AC144373/c  
LOCUS  
DEFINITION  
Felis catus clone RP86-72M21, WORKING DRAFT SEQUENCE, 4 ordered  
pieces.  
AC144373  
VERSION  
AC144373.2 GI:31791074  
KEYWORDS  
HTG: HTGS PHASE2: HTGS\_DRAFT.  
SOURCE  
Felis catus (cat)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.

REFERENCE  
AUTHORS  
Antoniellis A., Ayele K., Beckstrom-Sternberg, S.M., Benjamin, B.,  
Blakeley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Carriaga, K.,  
Chu, G., Coleman, B., Coleman, H., Engle, D., Granite, S., Guan, X.,

Gupte, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Hu, P.,  
Hurt, B., Idol, J.R., Karlins, E., Kwong, P., Latic, P., Lee-Lin, S.-Q.,  
Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Mesello, C.,  
Merkel, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E.,  
Prasad, A., Reddix-Dugue, N., Schadtler, K., Schaefer, M.G., Shah, K.,  
Sison, C., Stancipop, S., Thomas, J.W., Thomas, P.J., Tsipouri, V.,  
Vogt, J.L., Wehrby, K.D., Wiggins, L., Young, A. and Green, E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 145962)  
Green, E.D.  
Direct Submission  
Submitted (10-APR-2003) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Galthersburg, MD 20877, USA  
3 (bases 1 to 145962)  
Green, E.D.  
Direct Submission  
Submitted (17-JUN-2003) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Galthersburg, MD 20877, USA  
On Jun 17, 2003 this sequence version replaced gi:29725788.  
----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: nisc.zoo@nih.gov  
----- Project Information  
Center project name: dat  
Center clone name: 072M21

The sequence data in this record represents an 'enhanced'  
version of a Phase 2 submission. Specifically, the indicated  
order and orientation of each sequence contig has been  
established using one or more of the following: read-pair  
data from individual subclones, overlaps with neighboring  
clones, alignment with available reference sequence (e.g.,  
human), and/or confirmation by PCR testing. In addition,  
the sequence assembly is based on at least 8x average  
coverage in Q20 bases and has been reviewed to rule out  
gross misassemblies, the low-quality ends of sequence  
contigs have been trimmed away, and each base is associated  
with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 145279 bases at least Q40  
Consensus quality: 145536 bases at least Q30  
Consensus quality: 145626 bases at least Q20  
Insert size: 145000; agarose-fp  
Insert size: 145662; sum-of-contigs  
Quality coverage: 10.85x in Q20 bases; agarose-fp  
Quality coverage: 10.81x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 4 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1  
\* 9313 9412: contig of 9312 bp in length  
\* 9413 9412: gap of 12747 bp in length.  
\* 22159: contig of unknown length  
\* 22160 22259: gap of unknown length  
\* 22260 83593: contig of 61334 bp in length  
\* 83594 83694: gap of unknown length  
\* 83694 145962: contig of 62269 bp in length.

FEATURES  
SOURCE  
1. 145962  
/organism="Felis catus"  
/mol\_type="genomic DNA"



QY 1293 GTGACAAATGTCGAAA---GTAGTACCTAATAAATATTTGATATGAACCACTGC 1849  
 DB 112274 GTGACAAATGTCGAAAAGTGTAGTACCTAATAAATATTTGATATGAACCACTGC 112215  
 QY 1850 ACTCTCTTGG---GAAAAAAGTAAATGATTAATCTCTCTTAAGAGTCTTAAGTCTCC 1905  
 DB 112214 ATTTCTGGGGGGGGGGGAGTAAATGATTAATCTCTCTTAAGAGTCTTAAGTCTCC 112155  
 QY 1906 AAAAGTGTAGGAAAAATTAATCTCTGTGGCTGGAACAGCTCTGTCTTCTGGCTGC 1965  
 DB 112154 AAAAGTGTAGGAAAAATTAATCTCTGTGGCTGGAACAGCT--TGTCTCTAGTGC 112097  
 QY 1966 TATAATTTGTAGGTTTTTAAATGATTAATGATTAAGCTGTGTGGCTCCCAAGCTAAG 2025  
 DB 112096 TATGTTGGCTTAGCTTTAAACAGTTCAATTTGATTAAGTCTGTGGCTCCCAAGCTAAG 112037  
 QY 2026 GTTGAAGATTGATTCCTCAAGAGGCCACTTCAATTTAGAGAACAAAAGCCCACTTCTC 2085  
 DB 112036 GTTGAAGATTGATTCCTCAAGAGGCCACTTCAATTTAGAGAACAAAAGCCCACTTCTC 111977  
 QY 2086 TGCTCCAGACCTTACCCCAATCCCTGCAAGTGTCTGGCCCTCGGTC--AAATGAGAA 2144  
 DB 111976 TGCTCCAGACCTTACCCCAATCCCTGCAAGTGTCTGGCCCTCGGTC--AAATGAGAA 111917  
 QY 2145 CTGGCAAGGAACTAAGAGAGTGCACAGTACTAGAGAGTAAAGTAAAGTAAAGTAAAG 2204  
 DB 111916 CTGGCAAGG---GTTGCAACCAATCGTAG 111889  
 QY 2205 ACTACTGAGAAAGCAAAAAATGGGACCCCTTCAATGATGTGTCTTCTCTGTGT 2264  
 DB 111888 TATTTGGGAAATGTAAACCGAACAACCTTATATATATGCTCTTCACTTATATGTC 111829  
 QY 2265 TCACAAATGCTCGAATATATTAATTAAGAGAGTAAATACATATTTTCTTTAAACACT 2324  
 DB 111828 TGACAGTATTTGATTAATTAATTAATTAAGAGTAAATACATATTTTCTTTAAACACT 111770  
 QY 2325 GGAAGGCTGAGGAAAACTTTG-----TTACCAATCAATAAATTCATATCTT 2371  
 DB 111769 GGAATCTGAGGCAACCTGTCTGTGCTGATGCAATGCGAATCGAATAACCATGTGCTT 111710  
 QY 2372 CTAAGTCAATTAATGTTTCTTAAGATCAAAATAGTGCATATCTTCTTTGATTAAC 2431  
 DB 111709 CTTATTC--TGAGTTCAGAGATTTTCTTCTAGTGCATATCTTCTTTGATTAAC 111652  
 QY 2432 AATGAAAAACACATCTCTGAGCAATATTAATCTGCAACTTGAAGTAAAGTAAAGT 2491  
 DB 111651 AATGAAAAACACATCTCTGAGCAATATTAATCTGCAACTTGAAGTAAAGTAAAGT 111592  
 QY 2492 AATGCTAGTCAATGAACTGAAATACAAATTTCAATGAAATAA---GATATTAAT 2546  
 DB 111591 AATGCTAGTCAATGAACTGAAATACAAATTTCAATGAAATAA---GATATTAAT 111532  
 QY 2547 TAAAGTAAATCTGAGCAATTAATTAATTAAGTAAAGTAAAGTAAAGTAAAGT 2603  
 DB 111531 TAAAGTAAATCTGAGCAATTAATTAATTAAGTAAAGTAAAGTAAAGTAAAGT 111472  
 QY 2604 AATTAATCTGAGGAAACAGTGTCTCAATTAATGAGCAAAATCTTACTAGTATGAC- 2662  
 DB 111471 AATTAATCTGAGGAAACAGTGTCTCAATTAATGAGCAAAATCTTACTAGTATGAC- 111412  
 QY 2663 -----AGTCTTTCATTTAAATGCTTCTGAAATAATGCTGATTTCTAATTAACA 2713  
 DB 111411 ATCTTAGCTTTCTTAAATCAGGCTTCTGAAATAATGCTGATTTCTAATTAACA 111352  
 QY 2714 AGAC---TAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2770  
 DB 111351 CGGACTTAAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 111292  
 QY 2771 AATAGTAAATCAATTTATTTTCTGAGGAAAGCAATCACTTTTAAGATGA 2830  
 DB 111291 AATAGTAAATCAATTTATTTTAAAGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 111232

QY 2831 GTGT-AAATTAAGATTATTCATTAATTAATTAATTTTAAAGTTTCAATATAAGATG 2889  
 DB 111231 GTGTAAATTAAGATTATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 111175  
 QY 2890 AATTAAGATTATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2943  
 DB 111174 AATTAAGATTATTAAGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 111115  
 QY 2944 TCACATACAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3003  
 DB 111114 TCACATATATCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 111055  
 QY 3004 GCTCACCTTGTACTGTAAACAAATATCTGTTGTGACTGTGTGACAGACAGGTTTAAAC 3063  
 DB 111054 GCTCACCTTGTACTGTAAACAAATATCTGTTGTGACTGTGTGACAGACAGGTTTAAAC 110995  
 QY 3064 TCTGACAGCGAGATTCTATTTGTGAGCAAGAGCCCAATCATGATCTTACAGACACTTGTCT 3123  
 DB 110994 TCTGACAGCGAGATTCTATTTGTGAGCAAGAGCCCAATCATGATCTTACAGACACTTGTCT 110935  
 QY 3124 CATCAAGATTGGAATTAATAAAGCCACTTGAATATAGATTAATAAGATTCACTGTGTG 3183  
 DB 110934 CATCAAGATTGGAATTAATAAAGCCACTTGAATATAGATTAATAAGATTCACTGTGTG 110875  
 QY 3184 CAAGTTGCTCTGACAGTGGGAGGAGCAATTAACGTTGGCTTGGCTTCAAAAGCAAA 3243  
 DB 110874 CAAGTTGCTCTGACAGTGGGAGGAGCAATTAACGTTGGCTTGGCTTCAAAAGCAAA 110815  
 QY 3244 AGAAAGTAAAGGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 3303  
 DB 110814 AGAAAGTAAAGGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 110755  
 QY 3304 CAAAAAGTCAAAATCTCTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3363  
 DB 110754 CAAAAAGTCAAAATCTCTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 110695  
 QY 3364 GATCTGAATGAAACAGCGAGCAAG 3389  
 DB 110694 GATCTGAATGAAACAGCGAGCAAG 110669

RESULT 8  
 AC073120/c 43877 bp DNA linear PRI 07-NOV-2001  
 LOCUS  
 DEFINITION Homo sapiens BAC clone Rpi1-612D17 from 2, complete sequence.  
 ACCESSION AC073120  
 VERSION AC073120.5 GI:15638891  
 KEYWORDS  
 HTG.  
 SOURCE  
 Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 1 (bases 1 to 43877)  
 Sultson, U.E. and Waterston, R.  
 Toward a complete human genome sequence  
 Genome Res. 8 (11), 1097-1108 (1998)  
 JOURNAL MEDLINE  
 PUBMED 99063792  
 REFERENCE  
 2 (bases 1 to 43877)  
 Nguyen, C., Maupin, R., Dignan, G. and Wedgeworth, P.  
 The sequence of Homo sapiens BAC clone Rpi1-612D17  
 Unpublished  
 JOURNAL REFERENCE  
 3 (bases 1 to 43877)  
 Waterston, R.H.  
 TITL Direct Submission  
 JOURNAL Submitted (08-JUN-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE  
 4 (bases 1 to 43877)  
 Waterston, R.H.  
 TITL Direct Submission  
 JOURNAL Submitted (18-SEP-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,



REFERENCE MO 63108, USA  
 5 (bases 1 to 43877)  
 AUTHORS Waterston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (07-NOV-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 COMMENT On Sep 18, 2001 this sequence version replaced gi:114043001.

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: MUGSC  
 Web site: <http://genome.wustl.edu/gsc>  
 Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
 ----- Summary Statistics  
 Center project name: H\_NH0612D17

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:  
 Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:  
 The RPI1-11 human BAC library was made from the blood of one male donor, as described by Osogawa, K., Moon, P. Y., Zhao, B., Frengen, B., Tatenno, M., Catanesse, J. J. and de Jong, P. J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)

VECTOR: pBACe3.6  
 NEIGHBORING SEQUENCE INFORMATION:  
 The clone sequenced to the left is RPI1-16H9; the clone sequenced to the right is RPI1-128011, 200 bp overlap. Actual start of this clone is at base position 31717 of RPI1-16H9; actual end is at base position 114077 of RPI1-128011.

Data from AC011941 was used to finish this clone.

#### FEATURES

SOURCE  
 1. 43877  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="2"  
 /map="2"  
 /clone="RP11-612D17"  
 /clone\_11b="RP11-11"  
 repeat\_region  
 327..350  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 1135..1211  
 /rpt\_family="L1"  
 repeat\_region  
 1198..1234  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 1654..1679  
 /rpt\_family="(A)n"  
 repeat\_region  
 1682..1999  
 /rpt\_family="Alu"  
 repeat\_region  
 1976..2008  
 /rpt\_family="(A)n"  
 repeat\_region  
 2020..2163  
 /rpt\_family="L1"  
 repeat\_region  
 2175..2277  
 /rpt\_family="L1"  
 repeat\_region  
 2278..2562  
 /rpt\_family="Alu"  
 repeat\_region  
 2563..2623  
 /rpt\_family="L1"  
 repeat\_region  
 2633..2720  
 /rpt\_family="ERV1"  
 repeat\_region  
 2721..3136  
 /rpt\_family="L1"  
 repeat\_region  
 5998..6019  
 /rpt\_family="(TTTC)n"  
 repeat\_region  
 6021..6196  
 /rpt\_family="(TTC)n"  
 repeat\_region  
 6189..6496  
 /rpt\_family="Alu"  
 repeat\_region  
 6576..6626  
 /rpt\_family="MIR"  
 repeat\_region  
 9551..9579  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 9783..9829  
 /rpt\_family="MIR"  
 repeat\_region  
 13375..13519  
 /rpt\_family="MIR"  
 repeat\_region  
 13619..14081  
 /rpt\_family="MERL\_type"  
 repeat\_region  
 14106..14113  
 /rpt\_family="L2"  
 repeat\_region  
 15315..15662  
 /rpt\_family="ERV1"  
 repeat\_region  
 15723..15868  
 /rpt\_family="ERV1"  
 repeat\_region  
 15922..16087  
 /rpt\_family="L1"  
 repeat\_region  
 16029..16085  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 16325..16624  
 /rpt\_family="L1"  
 repeat\_region  
 16894..16925  
 /rpt\_family="MALR"  
 repeat\_region  
 17154..17527  
 /rpt\_family="ERV1"  
 repeat\_region  
 18287..18333  
 /rpt\_family="MIR"  
 repeat\_region  
 18931..18972  
 /rpt\_family="(TTTA)n"  
 repeat\_region  
 18946..19246  
 /rpt\_family="Alu"  
 repeat\_region  
 21338..22611  
 /rpt\_family="L1"  
 repeat\_region  
 22593..22614  
 /rpt\_family="AT\_rich"  
 repeat\_region  
 22814..23028  
 /note="match to EST AA476419 (NID:g2204630) zx02b02.s1"  
 repeat\_region  
 22820..23263  
 /note="match to EST N95327 (NID:g1267617) zb62e10.s1"  
 repeat\_region  
 22967..23324  
 /note="match to EST N95327 (NID:g1267617) zb62e10.s1"  
 repeat\_region  
 23587..23944  
 /note="similar to Bos taurus EST BE749870 (NID:g10163862)"  
 repeat\_region  
 24073..24534  
 /note="match to EST H92027 (NID:g1087605) y682d10.r1"  
 repeat\_region  
 24352..24757  
 /note="match to EST AA446796 (NID:g1259461) zw89f05.r1"  
 repeat\_region  
 24607..24757  
 /note="match to EST AA476520 (NID:g2204731) zx02b02.r1"  
 repeat\_region  
 25062..25128  
 /note="match to EST W07375 (NID:g1281376) za96d04.r1"  
 repeat\_region  
 25860..26105  
 /rpt\_family="GA-rich"  
 repeat\_region  
 26105..26147  
 /rpt\_family="L1"

```
repeat_region /rpf_family="(TA)n"
26712..26739
/rpf_family="AT_rich"
misc_feature 27181..27553
/note="match to EST W07375 (NID:g1281376) za96b04.r1"
misc_feature 27181..27199
/note="match to EST AA476520 (NID:g12204731) zx02b02.r1"
misc_feature 27465..27554
/note="match to EST BE296886 (NID:g9180453)"
misc_feature 27483..27554
/note="match to EST BG194829 (NID:g13716644)"
misc_feature 29343..29629
/note="match to EST BE296886 (NID:g9180453)"
misc_feature 29343..29564
/note="match to EST BG194829 (NID:g13716644)"
repeat_region /rpf_family="AT_rich"
30260..30294
/note="match to EST BG194829 (NID:g13716644)"
repeat_region /rpf_family="MIR"
31554..31764
/rpf_family="MIR"
repeat_region 32002..32378
/rpf_family="MER2_type"
repeat_region 32379..32588
/rpf_family="L1"
repeat_region 32589..32908
```

Query Match 45.3%; Score 1537; DB 9; Length 43877;  
Beet Local Similarity 73.2%; Pred. No. 1.3e-261;  
Matches 2554; Conservative 0; Mismatches 750; Indels 187; Gaps 38;

```
1 TGCTGCTCCGGAAGCATGGAAGTTGGAATCCCGGACGTGGAAGGAAGAAACACCTTC 60
33032 TTCTATTTGGGGCTCAGGAAGTTGGCAATCACTGCACTGGAAGAAAGAAATTAACCTTA 32973
61 TTGAATTTCTGAGTACCTCTTAATTCATTCATGCTGACCTCCGGA-----GATTGG 114
32972 CTTAAATTTCTTCAAGTCTTCTTCACTCACTCAATGCTGCTGCTGCTGAGGAAGTTGATTAG 32913
115 ATAGAGCTGCTGCTATTCATTCACAGTGTATGTTCTAACCAATCACTGCCAACA-TGA 173
32912 ATATAGTCATTTCTCCCTATTCATGATGTTATGTTCTAATGAAGCATTTGCCAACACTGA 32853
174 ATAGAGTCTCTGGAACACCTGCCCTAGGGGAAGTAAGGTTAGATTCCTCCGACGCT 233
32852 GTTAGCAATATTTGAATGATGTTCCAGGGGAAAGAGGTTAGTGAAGCTCTCG--- 32796
234 CTGCTCAAGTTTGTGTTAACCAATCAATTAATTAACCTGTTTGTGTCATTTCTGTTT 293
32795 GTCAATACATTTTACATCAACCAATCAATTAATTAACCTGTTTGTGTTATGTTTGTGTTA 32736
294 AAAATATCTTATTTAATGCTGCTAATTTCTTCAACATTTGGTTCAACCAAGAAAG 353
32735 CAAATTA-CATTAATTAATTAATTAATTTGTTCAATTAACCTGAACCTCAAGCCA---G 32681
354 CCCATTAATGGAAGCCGTAATGAGCTTAACATTAACACATTTGTTTCTATGAGGA 413
32680 CAGACATTAATCACTGAGCCCTTAATGATGCTTATCTAGACA---TGCAATTTTTCATGAG 32624
414 AAAATTTTCTGCTGCTGCAACAGCCTTCTTGCTTAATTAATTTGAGCAAAATATACA 473
32623 AACTTTTTCCTTACGATATCAAGCCTT-----TTAAATTTGTTGTAATTAATTAACA 32569
474 TAAATGAACTGACATTAATTAATTAATTTAATGATTTAATCTGTAAGTTCAAGTGCATTAAGTA 533
32568 ACATTTAGCA-----TCCTTAACCATTTTATGAGGTATACAGTTGCGTGCATTAAGCA 32518
534 CACTTACCTGCTGGAAGCAATATGATGAACATTCATCTCTAGAACCTTTTATCTTCGCG 593
32517 CATTCACATGTTGTGTAATCAATCAACCAATTAATTTCAAGAAATTTTATCTTCCCA 32458
594 AATTGAAATCTGCTATTTATGCAAGTATGCTTCCCAATCAACCGACCTTCCTC 653
32457 GACTG-AACTCTGATCTATACACAGTAAGTAAGTACCTCA-----GTGCTCAAC 32408
```

```
654 CAGCCCCCGGACCAACCATCTTCTTCCATGACAGTCACTCTGTGCTTAGAACA--- 710
32407 CAGTCCCTGGCAACCAACCATCTCTTCTTCCATGACAGTCTCTGTGATAGAACTAG 32348
711 -----CAGCCTTCAACACTACGCTTGGGGGCACTGT-----AAGCAACAGATC 756
32347 GAAACCAACGAGCACTGACACTATGCTTGGGGCCATTTTAAAAAGCAAAATCAAT 32288
757 ACTCCCTACCGCCACCAATGACACAAATAATTAATAAGCATGATGATGATTC 816
32287 AAGAGGACATTAATAAAGAAAGCAAAATATGTAAGAAATGCACTAATAGACGG 32228
817 AAAAAAGGCTGTTGCT--AAGTATGAGGCTGAAGC---AAGCAAGAAATGACTAGT 871
32227 AAAAAAGGAATTTTATATATATGAAGAGCTGAAGAAAGGGGAACCTGCTGTT 32168
872 TGACCTGAGCTGGATCCTGTGTGTG--AAGCTCAAAATTTTCAATGTTCTGTGAT 929
32167 TGACCTGATCTGGAACTGTGTGCTGATAGACTCAAAATTTTGGCGCTGTGAT 32108
930 AAGCAAAATGCTTATTAAGCACTGTAAGATTTGATTAAGTAAGTAATTAATCTAG 989
32107 GCCAGCAATGACATGAAGAA---TGCTAGGAATATGATGATTCATGATTAATTTAGC 32052
990 CAAGCATTAATGTCAGACGCGGATCATGAATTAAGCACTGACAT--GTGAAA 1047
32051 AAGTAGCAATTTGTGAATACAGAAATCAATGAATTAAGAAATTTGCTGTAGCGGAA 31992
1048 TGATATCTTGTGTTCTTATTTCCAGGAGTAAGGAAAGGCG-----T 1093
31991 TGACAACTTGTGCTCACTTTTTCAGGTGATTAAGAAATTAAGACCTGAACATCTTGT 31932
1094 CACAGGCTGCTTACACCAATTTTACAGAGCTAGCTATGTCAGTCCG----- 1144
31931 AACCTGCTGCTTGAAGAAATTTTACTTGCTCAAGGCTGAAGAAATGAGCTTGTGAC 31872
1145 ---TAGCTGGCAATTAACAAGTGAAGATTTATGTTCAATGTGAGAGTGAATTAACA 1201
31871 TGATTAATTTGAGCTATGACCTGAAGAGTCTGATGATGATGAGATTAATTTAAGCA 31812
1202 TAATCTAACCCCTTCTGCAATTAACAAGAGCAAGTCAATTAAGTCAATTAATTAATTA 1261
31811 TAATCTAACCCCTTCTGCAATTAACAAGAGCAAGTCAATTAAGTCAATTAATTAATTA 31752
1262 CTTACTATGACAGGCACTGTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1321
31751 CTTACTATGACAGGCACTGTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTA 31692
1322 CAACACTCTATGAGAGAGCTGAAGTTAG---AAGTATCTCATTCATTAATTAACA 1376
31691 CAAAACCTTATGAGAGAGCTGAAGTTAGAGTTAAGTATCTCATTCATTAATTAATTAACA 31632
1377 GT-----GGCAATGAGATGTAAGTCAAGTCAATCAATCCAGAGCTGAGATC 1428
31631 GTTAGAAGTGCAGAAAGTTGAGATTTGAATCTAGGCTTATCTGATCTCAAGAGCTGAGTTC 31572
1429 CCAATTCCTACACAAATCTATCAAGTAAAGGAAAGAAAGATTTGATTTGCTCAGAG 1488
31571 TCATTTCACTGATATCAATTCATTAAGCAATTAATTAATTAATTAATTAATTAATTAATTA 31512
1489 TGTATAGGGCATATGTTACA---ATTATTAATTAACAAGATTTATATGTTGAAAAATA 1545
31511 TGTATATGATGATGTTTAAACAATGATTAATTAATTAAGATTTTAAACATTTGAAAAATG 31452
1546 AATTATCAAAATTAATTAATTAATTAAGCTATTAATTAATGCTCCGGAACAAAGACT 1605
31451 AATTATCAAAATTAATTAATTAATTAAGCTATTAATTAATGCTCCATTAACAAAGACT 31392
1606 ATCTGAATCTTCAAGGAGCTGTTGTGCTGTTTCTTAATCTTAAATGATGAG 1665
31391 ATCTGAATCTTCAAGGAGCTGTTGTGCTGTTTCTTAATCTTAAATGATGAG 31333
1666 CAAATTAATGATTAATTAATTAAGGCA-TTTTTTCTCAAGAGATGATGATGATGATGATGAT 1724
```



REFERENCE 2 (bases 1 to 160415)  
 AUTHORS Green, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (06-MAR-2003) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 REFERENCE 3 (bases 1 to 160415)  
 AUTHORS Green, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-MAR-2003) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 On Mar 20, 2003 this sequence version replaced gi:28866993.  
 COMMENT ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.zoemhgrf.nih.gov  
 ----- Project Information  
 Center project name: daf  
 Center clone name: 007812

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies; the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; Version 0.990319  
 Consensus quality: 160260 bases at least Q40  
 Consensus quality: 160300 bases at least Q30  
 Consensus quality: 160312 bases at least Q20  
 Insert size: 164000; agarose-fp  
 Insert size: 160315; sum-of-contigs  
 Quality coverage: 11.94x in Q20 bases; agarose-fp  
 Quality coverage: 12.21x in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 105552: contig of 105552 bp in length  
 \* 105553 105652: gap of unknown length  
 \* 105653 160415: contig of 54763 bp in length.  
 Location/Qualifiers  
 1. 160415  
 /organism="Papio anubis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9555"  
 /clone="RP41-7812"  
 /clone\_1id="RP41"  
 1. 105552  
 /note="assembly\_fragment  
 clone\_end:T7  
 vector\_side:left"  
 1. 51269  
 /note="clone overlaps with GenBank Accession Number  
 RP41-32909 (center project name daf)"  
 105653. 160415  
 /note="assembly\_fragment  
 clone\_end:SP6

misc\_feature  
 misc\_feature  
 misc\_feature

| ORIGIN                     | vector_side:right"                                                           |
|----------------------------|------------------------------------------------------------------------------|
| Query Match                | 45.3%; Score 1536.4; DB 2; Length 160415;                                    |
| Best Local Similarity      | 73.5%; Pred. No. 1.3e-261;                                                   |
| Matches 2564; Conservative | 0; Mismatches 741; Indels 183; Gaps 40;                                      |
| QY                         | 1 TGCTGCTCCGAGCCATAGAGAGGTGCAATCCCGGACCTGAGAGAAACACGCTC 60                   |
| DB                         | 127843 TTCTATCTGCGGGCTTCGAAAGGTGCAATCACTGCGACCTGAGAGAAATTAACCTTA 127784      |
| QY                         | 61 TTGAAATTTCTTGAGTACCTCTTAAATTCATTCATGCTGACCTCCGA-----GATTGG 114            |
| DB                         | 127783 TTTAAATTTCTTGAGTACCTCTTAAATTCATTCATGCTGACCTCCGA-----GATTGG 127724     |
| QY                         | 115 ATAGAGGCTACCTCATTAATTCACAGGTGATGTTCAACCATTCACCTGCCACA-TGA 173            |
| DB                         | 127723 ATATATGTCATTTCTCCCTATTCATACATGTTATGTTCTATTAAGTCAATTGCGAACACTGA 127664 |
| QY                         | 174 ATAAATGATTCCTGAAACCACTGCCCTTAGGGGAACCTACAAAGTTAGATTCCCGTCAAGCT 233       |
| DB                         | 127663 GTTAGCAAAATATGTAATGATTTGCCAGGGGAAAAACAGGTTAGTTAGACCTCTG--- 127607     |
| QY                         | 234 CTGCTACGTTTTTGTGTTAACCATCAATTAATACCTTTGTTGTGTCATTTCTGTTT 293             |
| DB                         | 127606 GTCAATACATTTTTCATCAACCAATCAATATTAACCTGTTTATGTTGTTTGTGTTTA 127547      |
| QY                         | 294 AAATATCTTATTTAATATAGCTAGTCTGTAATTTCTTCAACATTTGTTTCAACACCAAAAG 353        |
| DB                         | 127546 CATATA-CGTTATTTAATATATATATGTCATTTCAACAGAACTACAGCCACACAGC 127488       |
| QY                         | 354 CCTATTAATCTGAAAGCCCTGAAATGAAGCTTACATTAACACACATTTGTTTCTATGAGA 413         |
| DB                         | 127487 ACCGTAATC-----AGCCGTGAATGATGCTTATCTACACACGCAATTTTTC---ATAAG 127435    |
| QY                         | 414 AAAATTTTCTTCAATCTGCGCCACAGCTTCTGCTTAAATTTGTGACAAATATATCA 473             |
| DB                         | 127434 AATTTTTTCCCTTAGGCATATCAACACCTT-----TTAAATATGTTG--TAAATATATCA 127382   |
| QY                         | 474 TAACATGAACCTGACTATTTATTTAATGATTTTAACTGATGTCAGTTCAGTGACATTAAGTA 533       |
| DB                         | 127381 TAACTTTAGATC-----TTAACATTTTAAAGTGTACAGTTCAGTGACATTAAGCA 127329        |
| QY                         | 534 CACTTACCTTGCTGAGAACTATGATCAACATTCATCTAGAACTTTTGTATCTTCTCG 593            |
| DB                         | 127328 CATTACACATGTTGTATACATCATCATCATCTTGGAATTTTCACTTCCAG 127269             |
| QY                         | 594 AATTGAAACCTGATCTATATGACAGTACCTTTCCCATCAACCCGACACCTTCTCTC 653             |
| DB                         | 127268 ACT--GAAACTCTTATCTATACACAGTAACTAACCCCTCAGTCCAGCACCTGGCAAC 127211      |
| QY                         | 654 CAGCCCCCGGACACCATCTCTTTCATGACATGCACTCACTGCTGCTAGAACACAG 713              |
| DB                         | 127210 CACATGCTACTTCTATATGACAGCTTTCTTGATATGAGAACATGAGAAC--CACACAG 127152     |
| QY                         | 714 CCCTTCAACACTAGCTGTTGGGGGCA--CTGTAGCAACAGAGTACCTCTTACCGCAC 772            |
| DB                         | 127151 CAGCTGACACTATGCTTGGGGGCAATTTTAAAAACCAAAATCAATTAACGAGGACATA 127092     |
| QY                         | 773 AAATGCA----CACAAATATTAATAAGCATGTGTGCAATTCATTCGAAAAAGGGTGT 828            |
| DB                         | 127091 AAAAAAGAGCAAAAATACGTGAAAAACATGCACTAAATAGCCGAAAAAGGGAAAT 127032        |
| QY                         | 829 TGCT--AAGTATGAGGCTGAAC---AAGCAGAGATATGACTAGGTTGACCTCAGCTG 883            |
| DB                         | 127031 TGTATATGATGATGAGCTGAACATTAAGGTGAAACCTGCTGTTTATACCTCATCTG 126972       |
| QY                         | 884 GGATCTGTGTGTGG--AAGCTCAATTTTCCATTTGTTCTGTGCAATGCACAAAATGC 941            |
| DB                         | 126971 GGAACCTGTGTGTGACAGAGACTGGAATTTTTCGCGCTGTGGAATGCAAGTAATGA 126912       |
| QY                         | 942 TTATTAAGACATGTAAAGATGATTATTAAGATTAAATTCACGAAAGACATTAAT 1001              |

Db 126911 TTGAAAAAGCTGAGATATTGAGTTTCATGATTAATTTGAGC---AAGAGGCAAT 126856  
Qy 1002 GTGCAGACGCGGATCCATGATTAACGAGACTGACAT--GTGAAATGATTAATCTTTG 1059  
Db 126855 TTGTGATACGAAATCATGATTAATGAAATTTGCTGTAGTGAATTCACATCTTTG 126796  
Qy 1060 TTTCCTTTATTCAGGAGTAAGGAAAGCGC-----TCACAGGGCTGCC 1105  
Db 126795 TTCACTTTTTTCAGGTAGTAAGATGAAGAGCTGGAACTATGTTTATCTGGCTGCC 126736  
Qy 1106 TTACACCACTTTTA-----CTAGAGACTGAGCTATGCTAGTGGTGTGG 1151  
Db 126735 TTGAAATTTTTCCTTGCTCAGACAGACTGAAAGGTAGACTTGTGTGCT--GATTAATGG 126677  
Qy 1152 CAATTACAACTGAAGAGAGTTCTAGTTCATGTGAGATGAATTAACATTAATCTGAC 1211  
Db 126676 CAGCTATACCTTGAGAGAGTTCTAGTTCATGTGAGATGAATTTTTCAGATTAATCTGAAA 126617  
Qy 1212 CCCCTCTGATGAAACAGAGACTAGTACTCAAGTACAGTTATCACTTACTATAT 1271  
Db 126616 TCCTTCTGATTAACAAAGAGAGAGCACTCAAGTCCAGTTATCAATTAATTAATG 126557  
Qy 1272 GACAGGACTGTATCAACAATTTATGATGATTTATGATTAATCATGCCCCCACTGTA 1331  
Db 126556 GACAGGTGTATCATTCAGCAATTTATCATGATTTATTAATTAATATCCCCCAAAACCTTA 126497  
Qy 1332 TGAGGAGCTGAAGGTAGAG---AAGTATCTGATTCATTAATTAACAGT----- 1378  
Db 126496 TGAGGAGCTGAAGGTAGAGGTGAGAGGTGAGATCTCATCATTAATTAATTAAGTGAAGTG 126437  
Qy 1379 GGCAGAACTGAGATCTGAACCTGAGTCTATCCAACTCCAGAGCTGAGATCCCAAT----- 1433  
Db 126436 GCAAGTGTGAATTTGAATCTGAGGTCTATCTGACTCCAGAGCTGAGTTCATTAATTAAC 126377  
Qy 1434 TGCTACACAAATTTCTATCAAGTTAAAGGAAAGGATTTGATTTGCTCAGAAAGTAT 1493  
Db 126376 TGCTATGCAATTTCTAAGCATTTAAAAAAGTTTGAATTTGATTTGCAACTGTAT 126317  
Qy 1494 AGGGGATATGTTTCA---ATTATTAACATTAACAAGATTTATATGTGAAATAATTT 1550  
Db 126316 AGATGCAATTTTACATGATTAATTTCAATTTCAAGATTTTACATTAATTAATTAATTT 126257  
Qy 1551 ATCAAAACAATTAACCTTTAAGGCTGATCTAATATCTGCTCCGCAACAAAGACTATCTG 1610  
Db 126256 ACCAAACAATTAACCTTTAAGGCTGATCTAATATCTGCTCCGCAACAAAGAGATCTG 126197  
Qy 1611 AAATCTTACAGGCACTGCTGTTGTGTCTGTTTCTTTAATCTTTAATGATGGCAAT 1670  
Db 126196 AAATCTC-TCAGGGCACTGCTGTTGTGTCTGTTTCTTTAATCTTTAATGATGGCAAT 126138  
Qy 1671 CTAATGCAATTAAGGCA-TTTTTCTCAAGAGATGATGATACCTCTTAAGAAATTTG 1729  
Db 126137 CCAATGCAATTAAGGCAATTTTTTCTCAAGAGATGATGATACCTCTTAAGAAATTTG 126078  
Qy 1730 ATGAAATGCAATTAATTTTACAGGCTACTGAGTTGCAATTTAAGTCACTGAGGCAATTA 1789  
Db 126077 ATGAAATGCAATTAATTTTACAGGCTACTGAGTTGCAATTTAAGTCACTGAGGCAATTA 126018  
Qy 1790 TTAAGTCAATGTCGCAAA---GTAGTCACTTAATAATAATTAATTTGATGACAC 1846  
Db 126017 TTAAGTCAATGTCGCAAAATGTCGCAATTTAATAATAATTAATTTGATGACAC 125958  
Qy 1847 TGCACTCTCTGGGGGAAAAAGTATGATTAATCTCTGAGATGCTGAGCTTCCCA 1906  
Db 125957 TGTATTTCTCTGGGAAAAAGTATGATTAATCTCTGAGATGCTGAGCTTCCCA 125898  
Qy 1907 AAAGTAGAGAAAAATTAATCTCTGTCGCTGAGAAACAGTTCTGTTTCTGTGCT 1966  
Db 125897 AAAGTAGAGAAAAATTAATCTCTGTCGCTGAGAAATCTTCTGTTTCTGTGCT 125838  
Qy 1967 ATATTGTTTAGTTTAAATGTTTCAATTTGATTAAGCTTGTGCTGCCAAAGTAAAG 2026  
Db 125837 ATGTTGCTTAGTTTCTTTAATGTTTCAATTTGATTAAGCTTGTGCTGCCAAAGTAAAG 125778

Qy 2027 TTGAGAGTTGATTCCTTACAGAGGCACTTCAATTTAAGAAACAAAAAGCCCATTTCT 2086  
Db 125777 TTGAAAGTTTATCCCTTACAGAGGCACTTCAATTTAAGAAACAAAAAGCCCATTTCT 125718  
Qy 2087 GCTCCAGACCTTAACCCCAATTCCTGCGAGGTGTCTGCTCCGCTCAATGAGAACT 2146  
Db 125717 GCTCCAGACCTTAACCCCAATTCCTGCGAGGTGTCTGCTCCGCTCAATGAGAACT 125658  
Qy 2147 GGCAGAGAACTACTAGAGAGTCCGACAGTCTAGAAAGTGAATAATGACTGACAC 2206  
Db 125657 TGGCAAGGGGTGAACA-----TATCAGAG 125631  
Qy 2207 TACTGAGAGAGAAAAATGGGCAACCTTCACTGATGATGTTCTTCCCTTCTGTGTC 2266  
Db 125630 TATTGGAGAAACAAAGAGTCAACCCCTTTATCATGATGCTTCTTCTTTAGTGTCT 125571  
Qy 2267 ACAATGCTCCGATTAATTTAACAAGGTAGATA-----ACTCAATTTTCTTTT 2318  
Db 125570 ACAATATCTGATTAATTTAAGAGAGATGATCTGCACTTTTATCTCTGCAAAATTT 125511  
Qy 2319 ACCAGTGAAGCTGAGAGAACTTTGTTACCCATCATTAATTCATATCTTCTAAGTC 2378  
Db 125510 GCTGCTGAAATCTGAGGCAACGTATTAAGCTCTGCAATGCCAGTTATTAAGTCAAT 125451  
Qy 2379 ATTCTAGTTTATCTAAGA-----TCAATAGCTGACAAATATCTCTTGTAAATAACA 2432  
Db 125450 ATCTTATTTCTATGTTCAAGAGATTTTCTACAGTGAATTAATCTCTTGTAAATAACA 125391  
Qy 2433 ATGAAAAACATCTCTGAGCAATTAATTTCTGCAACTTTAGATGAGAACTTTA 2492  
Db 125390 ATGAAAGAAACATCTCTGAGTATTAATTTCTGCACTTTAGAGTGAAGAA-----ATA 125336  
Qy 2493 ATACTAGTCAATTAATGAAATGAAATCAATTTTCAATTAATTAAGAAAT-----TATTT 2547  
Db 125335 ATAGCACTGAGTCAAAAGTCAATTAATTTTCAATTAATTAAGAAATCAATTAAGT 125276  
Qy 2548 AAAAGTATTCATGAGCAATTTAATTTA--AAGTGAAGTTTCAATTAATGTTAAGAT 2606  
Db 125275 AAAATATCTTCAATGCAATTAATTTAATTTAATTAAGTGAAGTCAATTTAAGAT 125216  
Qy 2607 TTAATCAGGAAACAGTTTCTCAATTAATTAAGCAAAATCTTTTACTAGTACAGTC 2666  
Db 125215 TTAATCA-AAAAACAAGTTTCTCAATTAATTAAGCAAAATCTTACTAGTACATTAAT 125157  
Qy 2667 TTTTCAATTAAGTC--TTCCTGAATTAATCTGATTTTCTAATTAATTAAGCACTAATAAT 2725  
Db 125156 TTAATTTTAAATCAAGTCTTCTAATTTTAAATTTTCTAATTAATTTGCACTAATAAT 125097  
Qy 2726 ATTTAATTAATCAATTAATTTAATTTTACTTCAATTTCTAATTAATTAATTAAT 2785  
Db 125096 ATTTAATTAATCAATTAATTTAATTTTACTTCAATTTCTTCAATTAATTAATTAAT 125037  
Qy 2846 TATTCACTTAATTAATTTTAAAGTTTCAATTAATTAATTAATTAATTAATTAAT 2903  
Db 124977 GACTTATTTAAATTAACAAGTT-----GTGTAAGATTAATTAAGTAAAGTAC 124928  
Qy 2904 -GTATGTTTATGTTAATTAAGTTTAAATTTTTCGATGCTCAATTAATTAATTAAT 2962  
Db 124927 AGTTTATTTATTCGCAATTAATTAATTTTGTGTTTCAATTAATTAATTAATTAAT 124868  
Qy 2963 TTCAATTAATTTATCTTTTAAAGATTAATTAATTAATTAATTAATTAATTAAT 3022  
Db 124867 TTTGTGATTTATTTCTTTTAAAGATTAATTAATTAATTAATTAATTAATTAAT 124808  
Qy 3023 AAAATATCTGTTGAGACTTGTGACAGAGGTTTAACTCTGACAGGAGATTAAT 3082  
Db 124807 AAAATATCTGTTGAGACTTGTGACAGAGGTTTAACTCTGACAGGAGATTAAT 124748





Db 43407 CAGTCCCTGGCAACACCATCTACTTTCATTTGACGCTTTCCTGTGATTAGAAACATAG 43466  
Qy 711 -----GAGCCCTTCAACACTAGCGCTGGGGGGACGTCT---AAGCAACGAGATC 756  
Db 43467 GAACACACGAGCAAGTACAGACTATGCTTGGGGGCGCATTTTAAAAAGCAAAATTCAT 43526  
Qy 757 ACTCCCTACCGCCCAACAATGCAACAAAAATATTAAGAAGCATGTGGCATATCGATTGC 816  
Db 43527 AAGAGAGCAATTAATAAAGAAAGCAAAATATGTGAAAACATGSCACTTAATATAGTGG 43586  
Qy 817 AAAAAAGGTCTTGTCT--AAGTAGAGGCTG---AAACAAGCAGAGAAATTTGACTAGT 871  
Db 43587 AAAAAAGGAATTTGTTTATAGATGAGAGCTGAAAAAATTAAGCGGAACCCGCTTGT 43646  
Qy 872 TGACCTGAGTGGATCTGTGTGTGG--AAGCTCAAAATTTTCATTTGCTGTGTGAT 929  
Db 43647 TGACCTGCTGGGAACCTGTGCGTCAGATAGGATTCAAATTTTGTGCTGTGTGAT 43706  
Qy 930 ACGCACAATGCTTATTAAGAAGCACTGAAGATTGATTGAAGTTAAGATTAATCTGAG 989  
Db 43707 GCCCGGAGATGACTGAAAA---TTCTAGGAATATGAGTTTCATAGATAATTTTAGC 43762  
Qy 990 CAAGACATTAATGTGCAAGCAAGGATCCATGATTAACGAGACTGACCAT--GTGAAA 1047  
Db 43763 AAGTAGCAATTTGTGATACAGAAATCATGAAATTAATGAATTTGTCTGTAGCGGGA 43822  
Qy 1048 TGATATATTTTGTTCCTTTATTCAGGCAATTAAGAAAGACGCTC----- 1094  
Db 43823 TGACAACTTTTGTTCATATTTTCCAGGTAAATTAAGATTAAGAGCTGGAACATGCTGT 43882  
Qy 1095 -ACAGGGCTGCTTACACCATTTTACTAGAGCTAGGCTATGTGATCGG----- 1144  
Db 43883 AACCTGGCTGCTTGAATAATTTTACTTCCCAAGGCTTAGAAGTAGGCTTTGTGAC 43942  
Qy 1145 ---TAGCTGGCAATTACAACCTGAAGAGTTCTAGTTCAATGTGAGATGAATTTAAC 1201  
Db 43943 TGATTAATGGCAGTATGACCTGAAGCAGTTCTAGTTCAATGTGAGATGAATTTAAC 44002  
Qy 1202 TAAATTCACACCCCTCTGATGAACAGAGACTAGTATCTCAAGTACCAAGTTATGATCA 1261  
Db 44003 TAAATTCACACCCCTCTGATGAACAGAGCAAGCAGCTCAAAAGCCAGTATCAATTA 44062  
Qy 1262 CTACTATATGACAGGACCTGACTCAACAATTTACATGATTTATTTGAATTAATGACCC 1321  
Db 44063 CTTACTATATGACAGGTGCAATTTACAGCAATTTACATGATTTAATTAATTCGCC 44122  
Qy 1322 CAACACTGATGAGAGCTGAAGGTTAG--AAGTATCTCAATTCATTTATACA 1376  
Db 44123 CAAAACCTATGAGAGCTGAAGTTAGGGAAGTTAAGTATCTCATCATTAACATA 44182  
Qy 1377 GT-----GGCAAACTGAGATCTGAACCTGAGTCTATCCAACTCCAGAGCTGAGATC 1428  
Db 44183 GTTGAAGGTGCAAGGTTGAGATTTGAACCTGAGTCTATCTGACTCCAGAGCTTAAGTTC 44242  
Qy 1429 CCAATTTGCTACCAATTTCTAATCAAGTTAAAGGAAAAAGGATTGATTGCTCAGAG 1488  
Db 44243 TCAATTTCACTGCTATGCAATTTCTAAGCATGTTTAAAAAAGTTGACTTACTTGGAAC 44302  
Qy 1489 TGTATAGGGGCAATATGTTACA---ATTATTAATTAACAAGATTATATGTTGAATA 1545  
Db 44303 TGTATAGATGATGTGTTACATGATCATTAATTTCAAAAGATTACATTTGAAAAATG 44362  
Qy 1546 AATTATTAACAACAAATTAACCTTTTAAGCTGATCTAATCTGCTCCGCAACAAAGCT 1605  
Db 44363 AATTATTAACAACAAATTAACCTTTTAAGACCGATCTAATATTTGCCATTAACAAAGT 44422  
Qy 1606 ATCTGAATCTTTCAGGGGATCTGGTTGTCTGAGTTTCTCTTAATCTTTAATGATGG 1665  
Db 44423 ATCTGAATCTTTCAGGGGATCTGGTTGTCTGAGTTTCTCTTAATCTTTAATGATGG 44481  
Qy 1666 CAATCTATGCAATTAATGTAAGGCA-TTTTTCTCAAGAGATGATGATCTCTTAAGA 1724

Db 44482 CAATTCACATGATTAATGTAAGGCAATTTTTTCTCAAGAGATGATGATCTCTTAAGA 44541  
Qy 1725 AATTGATGAATGATTAATTAATCTTTACAGGCTACTGATGTGATTTTATGCACTGAGCA 1784  
Db 44542 AATTGATGAATGATTAATTAATCTTTACAGGCTACTGATGTGATTTTATGCACTGAGCA 44601  
Qy 1785 GTAAATTAATGTAATGTAAGGCA---GTAGTGACTTAATAAATAATTAATTAATGATGA 1841  
Db 44602 GTAAATTAATGTAATGTAAGGCA---GTAGTGACTTAATAAATAATTAATTAATGATGA 44661  
Qy 1842 ACCACTGACCTCTTGG--GGAAAAAGTATGATTAATCTCTTGAAGATCTCTTACT 1900  
Db 44662 GCCACTGATTTCTCTTGGAAAAAATAATGATGATTAATCTCTTGAAGATCTCTTACT 44721  
Qy 1901 TCCCAAAAGTATGAGAAAAATTAATCTCTGAGGCTGAGAAACAGCTCTGTTCTTG 1960  
Db 44722 TCCCAAAAGTATGAGAAAAATTAATCTCTGAGGCTGAGAAATCTCTGTTCTTG 44781  
Qy 1961 CTGGCTATATTTGTTTATGATTTTAAATGTTTCAATTTGATTAAGCTTGTGCTCCCAAG 2020  
Db 44782 CTGGCTATATTTGTTTATGATTTTAAATGTTTCAATTTGATTAAGCTTGTGCTCCCAAG 44841  
Qy 2021 CTAAAGTTGAGATTTGATCTCTACAGAGGCACTTCAATTTAAGAAACAAAGCCCA 2080  
Db 44842 CTAAAGTTGAGATTTGATCTCTACAGAGGCACTTCAATTTAAGAAACAAAGCCCA 44901  
Qy 2081 TTCTGTGCTCCAGCCTTACCCCAATCCCTGCAAGGTCTGTGCTCCGCTCAATGA 2140  
Db 44902 TTCTGTGCTCCAGCCTTACCCCAATCCCTGCAAGGTCTGTGCTCCGCTCAATGA 44961  
Qy 2141 GAAACTGCAAAAGGATGATGAGAGGTGCAAGTACTAGAGATGAAGAAATGAGACTA 2200  
Db 44962 AGAAATGCAAAAGGAGTGAACATATGAG----- 44994  
Qy 2201 GCACTACTGAGAAAGCAAAATATGAGCACTTCAATGATGTCTCTTCTCTCT 2260  
Db 44995 -----TATGGAAGCAAAAGGTGCACTCTTATCAATGATGTCTCTCTCT 45048  
Qy 2261 GTGTTCACATGCTCCGATTAATTTTACAGAGGGATGA-----ACTACATTTT 2312  
Db 45049 GTGTTCACATGCTCCGATTAATTTTACAGAGGGATGA-----ACTACATTTT 45108  
Qy 2313 TCTTTACACATGAGGCTGAGAAACCTTGTATACCATATTAATTAATCAATCTTC 2372  
Db 45109 ATATTTACGCTGGAATCTGAGCAACCTGATTAATTAATTAATTAATTAATTAATTA 45168  
Qy 2373 TAACTCATTTATGTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2432  
Db 45169 TTCAATTAATTTATGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45228  
Qy 2433 ATGAAAAAACAATCTCTGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2492  
Db 45229 ATG-AAAAAACAATCTCTGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45282  
Qy 2493 ATACTAGCAATTTGAACTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2547  
Db 45283 ATGACACTGAGCAAAAGTTGATTAATTTTCAATTAATTAATTAATTAATTAATTAATTA 45342  
Qy 2548 AAAAGTAATTCATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2606  
Db 45343 AAAAGTAATTCATGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45402  
Qy 2607 TTAATTCAGGGAACAAGTTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2666  
Db 45403 TTAATTCAGGGAACAAGTTTCTCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45461  
Qy 2667 TTTTCATTTAAGTC-TTCTGAATTAATCTGATTTTCTAATTAATTAATTAATTAATTA 2725  
Db 45462 TTAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45521  
Qy 2726 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2784  
Db 45522 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 45581

```

QY 2785 CATTATTTTCTGAGGAGAAAAGATCACTTTTAAAGTGAAGTGAATTAAGT 2844
DB 45582 CATTATTTTCTGAGGAGAAATATTTTC-ATATTTTAAATATGATTAATTAAT 45640
QY 2845 TTATTCATTAATTAATTAATTTTAAAGTTTACATATTAAGATGAATTAAGTCTAAGT 2904
DB 45641 TGACTATTTTAAATTAATTAATTAAGATTTGATGAGATTAAGATTAAGT---TACAG 45696
QY 2905 TATATGTTATTTGTTAATAAAGTTTAAATTTTTCGATGTCATATACAGCTTTATTAAT 2964
DB 45697 TTATATTTATTTGCCAATATGACTTTTGTGTTTTCATATGTCATTAATTTTATTT 45756
QY 2965 CATATGTTATTTCTTTTAAAGATGATCAATGAATGATGATGATGATGATGATGATGAT 3024
DB 45757 TGATGATTTATTTCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45816
QY 3025 AATATCTGTTGTTGATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3084
DB 45817 AATATCTGTTGTTGATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 45876
QY 3085 GAGAGAGAGCCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3144
DB 45877 GAGAGAGAGCCATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 45936
QY 3145 AGCCACTTGAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3204
DB 45937 AGCCACTTGAATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 45996
QY 3205 CAGGATTAACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3264
DB 45997 CATGATTAATTAATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 46056
QY 3265 AAGAACAAG-GGAAAAAGATTGATGATTTTAAACATGCAAAATGCAAAATGCTGCTGCT 3323
DB 46057 AAGAACAAGAAAAAGATTGATGATTTTAAATCATGCAAAATGCAAAATGCTGCTGCT 46116
QY 3324 TTATTTTAACTTATTTATGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3383
DB 46117 TTATTTTAACTTATTTATGCTGATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 46176
QY 3384 GCAGAA 3389
DB 46177 GCAGAA 46182

RESULT 11
AC142555/c 248435 bp DNA linear HTG 21-JUN-2003
LOCUS Pan troglodytes clone CH251-526K6, WORKING DRAFT SEQUENCE.
AC142555
AC142555.3 GI:32140200
VERSION HTG, HTGS PHASE2, HTGS DRAFT.
KEYWORDS Pan troglodytes (chimpanzee)
SOURCE Pan troglodytes
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
1 (bases 1 to 248435)
Antonielle A., Ayele K., Beckstrom-Sternberg S.M., Benjamin B.,
Blakesley R.W., Bouffard G.G., Brinkley C., Brooke S., Carriaga K.,
Chu G., Coleman B., Coleman H., Engle J., Granite S., Guan X.,
Gupta J., Haghighi P., Han J., Hansen N., Ho S.-L., Hu P.,
Hutle B., Idol J.R., Karlins E., Kwong P., Latic P., Lee-Lin S.-Q.,
Legaspi R., Maduro Q.L., Maduro V.B., Margulies E.H., Matisello C.,
Markert B., McDowell J., Pegurigan C., Pearson R., Portnoy M.E.,
Prasad A., Reddix-Dugue N., Schandler K., Schueler M.G., Shah K.,
Simon C., Stanciford S., Thomas J.W., Thomas P.J., Troup J.,
Vogt J.L., Wehberby K.D., Wiggins L., Young A. and Green E.D.
NISC Comparative Sequencing Initiative
Unpublished
REFERENCE 2 (bases 1 to 248435)
JOURNAL Green E.D.
AUTHORS Direct Submission
TITLE

```

```

JOURNAL Submitted (04-APR-2003) NIH Intramural Sequencing Center, 8717
REFERENCE Government Circle, Gaithersburg, MD 20877, USA
AUTHORS Green E.D.
TITLE Direct Submission
JOURNAL Submitted (21-JUN-2003) NIH Intramural Sequencing Center, 8717
COMMENT Government Circle, Gaithersburg, MD 20877, USA
On Jun 21, 2003 this sequence version replaced gi:3104286.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@hghrl.nih.gov
----- Project Information
Center project name: chr
Center clone name: 526K06

The sequence data in this record represents an 'enhanced'
version of a Phase 2 submission. Specifically, the indicated
order and orientation of each sequence contig has been
established using one or more of the following: read-pair
data from individual subclones, overlaps with neighboring
clones, alignment with available reference sequence (e.g.,
human), and/or confirmation by PCR testing. In addition,
the sequence assembly is based on at least 8X average
coverage in Q20 bases and has been reviewed to rule out
gross misassemblies, the low-quality ends of sequence
contigs have been trimmed away, and each base is associated
with a Phrap-derived quality score.
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 248019 bases at least Q40
Consensus quality: 248241 bases at least Q30
Consensus quality: 248387 bases at least Q20
Insert size: 125000; agarose-fp
Insert size: 248435; sum-of-contigs
Quality coverage: 21.39x in Q20 bases; agarose-fp
Quality coverage: 10.76x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 248435; contig of 248435 bp in length.
Location/Qualifiers
1. 248435
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="CH251-526K6"
/clone_1fb="CH251"
1. 248435
/notes="assembly_fragment
clone_end:526
vector_side:left
vector_side:right
missing 77 clone end and on 3' end of insert"
1. 35330
/notes="clone overlaps with GenBank Accession Number
AC141847 clone CH251-555A6 (center project name dno)"

ORIGIN
Query Match 44.8%; Score 1519.6; DB 2; Length 248435;
Best Local Similarity 72.9%; Pred. No. 1.2e-258;
Matches 2540; Conservative 0; Mismatches 764; Indels 182; Gaps 38;

QY 1 TGCTGCTCCAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 60

```

Db 140181 TTCTATCTGGGGGATCAGGAAGGTGCAATCACTGCACCTGAGAAAGAAATAAACTTA 140122  
Oy 61 TTGAATTTCTGAGTACTCTGTAATTCATTCAGTGCAGCTCCGGA-----GATGG 114  
Db 140121 CTAAATTTCTCAGTCTCTCTCCACCAATCAATAGTCTCTAGGAAGTTGATAG 140062  
Oy 115 ATAGAGTCACTCATATTCACAGTGTATGTTCTACCAATCACTGCACA-TGA 173  
Db 140061 ATATAGTCAATTTCTCCATTCATATAGTATGTTCTATAAAGCATTTGCCAACACTGA 140002  
Oy 174 ATAAAGTATCTGGAACACTGCCCTTAGGGGAACCTAACAGGTTAGATTCCGTCAGCT 233  
Db 140001 GTTAGCAATATGGAATATGTTCCAGGGGAAAAACAGGGTTAGTTCAGCTCTG--- 139945  
Oy 234 CTGTCAGGTTTTGTTAAACCAATCAATTAATTAACCTGTTTGTGTGCAATTCCTGTTT 293  
Db 139944 GTCAATTAATTTACATCAACCAATCAATTAATTAACCTGTTTGTATGTTATTTA 139885  
Oy 294 AAAATATCTTATTTAATAGTAAGTATGTAATTTCTCAACATTTGGTCAACAACCAAG 353  
Db 139884 CAATTA-CATTTATTAATTAATATTTGTTCAATTTAACTGAACCTACAGGCCAACAG 139826  
Oy 354 CCTATTAATCTGGAAGCCCTGAATGAAGCTTAATTAACACACATTTGTTTCTATGAGA 413  
Db 139825 ACC---ATACTCAGGCTGTAATGATGTTATCTAGCATTA---TGCAATTTTTCATAG 139773  
Oy 414 AAAATTTTCTCTGATCTGTCGACAGCTCTTCTGCTTAAATTTGTGACAAAATATCA 473  
Db 139772 AACTTTTTTCTTAAAGCATATCAAGGCTT---TTAAATTTGTGTAATTAATCA 139718  
Oy 474 TAACATGAACCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 533  
Db 139717 ACATTTAGCA-----TCTTAACATTTTATAGTGTGATGTTGCGATTTAA 139667  
Oy 534 CACTTACCTGCTGTGAATCTATGATCAACATTCATCTCTAGAACCTTTTGTATCTTCTG 593  
Db 139666 CATTCACACTGTGTATTAACATCAACACATTCATCTCTAGAAATTTTTCATCTTCCA 139607  
Oy 594 AATTGAATCTCTGATCTATTTGACAGTATGTTTCCCAATCAACCGCACCTTCTCTC 653  
Db 139606 GACTG-AAACTCTGATCTATCAACAGTAATCACTCCCTCA-----GTGCTCAAC 139557  
Oy 654 CAGCCCCCGGACACCAATCTCTTTCATGACATCTCTGCTGCTAGAAC--- 710  
Db 139556 CAGTCTCTGGCAACCACTGCTACTTTCATTTGACGCTTCTCTGTATGAGAACATAG 139497  
Oy 711 -----CAGCCCTTCAACATCACTGCTGGGGGGGACCTGT---AAGCAACAGATC 756  
Db 139496 GAACACACGACGACGTCAGACTATGTTGGGGGCATTTTAAAGCAAAATCAAT 139437  
Oy 757 ACTCCCTTACCGGACCAAAATGACACAAATATTAATAAGCATGTGGCATATGCAATTC 816  
Db 139436 AAGAGCAATTAATAAAAGAGCAAAATATGTAATACTGTGCACTTAATATATATGCG 139377  
Oy 817 AAAAAGGAGTCTGCT--AAGTATAGGGCTG---AAACAAGGAGAAATGACTAGT 871  
Db 139376 AAAAAGGAAATTTGTTTATAGTATAGAGCTGAAAAAATAGGCGAAACCTGCTTGT 139317  
Oy 872 TGACCTCAGCTGGGATCTCTGTGTGTTG--AAGCTCAAAATTTTCATTTGTTCTGTGAT 929  
Db 139316 TGACCTGCTGGGAAACCTGTGCTCAATAGATTTCAAAATTTTGTGCTCTGTGAT 139257  
Oy 930 ACGCACAATCTTATTAAGACATGTAAGATTTGATTTGAAGTTAAGATTAATCTCAG 989  
Db 139256 GCCCGCAATGACTAAAAA---TTCTAGGAATATGAGTTTCAATAGATAATTTTGC 139201  
Oy 990 CAAGCATTAATGTGACAGCAGGATCATGATTAAGACAGCAGCAAT--GTGAAA 1047  
Db 139200 AAGTAGGCAATTTTGTGATACAGAAATCATGAATTAATGAATTTGTCTGTTAGCGGAA 139141  
Oy 1048 TGATATCTTTGTTTCTTTATTCAGGACGTAGAGAAAGCGCTC----- 1094

Db 139140 TGACAACTTTGTTCACTATTTTCCAGGTAAATAAATAAAGCTGACATGCTTGT 139081  
Oy 1095 -ACAGGCTGCTTACACCAATTTTACTAGAGAGTACCTATGTCAGTCG----- 1144  
Db 139080 AACCTGGCTGCTTAGAAAAATTTTACTTGTCTCAGAGGCTAGAAAGAGGCTTTGTAC 139021  
Oy 1145 ---TAGCTGGCAATTAACAACTGAAGAGTTCTAGTTCAATGTGAGAGATTAATTA 1201  
Db 139020 TGATTAATGGAGCTATGACCTGAAGCAGTTCTAGTTCAATGTGAGAGATTAATTA 138961  
Oy 1202 TAATCTCAACCCCTCTGCTAGAAACAGACATTAAGTCTCAATACCTAGTTATCAGTCA 1261  
Db 138960 TAATCTCAACCCCTCTGCTAGAAACAAAGAGCAGCACTCAATATGCAATTAATTA 138901  
Oy 1262 CTATCTATAGACAGGACCTGACTCAACATTTATCAATGATTAATTAATTAATTAATTA 1321  
Db 138900 CTATCTATATACAGGTGCTATTCAGCAATTTACATGCTTTTAATTAATTAATTAATTA 138841  
Oy 1322 CAACACTTATAGAGAGCTGAAGGTTAGAG---AAGTATCTCATTTCAATTAATTA 1376  
Db 138840 CAAAACCTATAGAGAGCTAAAGTTTAGGGAAGTTAAGTATCTATTCATTCATTAATTA 138781  
Oy 1377 GT-----GGCAACTGAGATCTGAATCTAGGCTATTCACACTCCAGACCTGAATC 1428  
Db 138780 GTTAGAGGTGCAAAAGTTGAGATTTGAATCTCAGGCTATCTGACTCCAGAGCTGAGTT 138721  
Oy 1429 CCAATTTGCTACAAATTTCTATCAAGTTAAAGGAAAAAGAGTTGATTTGCTCAGAA 1488  
Db 138720 TCAATTTCACTGCTATGCAATTTCTAGCATGTTTAAAAAAAGTTTGACTTATGGAAC 138661  
Oy 1489 TGATAGGGGCAATGTTTACA---ATTATTAATTAACAAAGATTTATATGTTAAAAA 1545  
Db 138660 TGATATAGTATGATGTTTACATGATCATACAATTCABAAATTAATTAATTAATTA 138601  
Oy 1546 AATTTATCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1605  
Db 138600 AATTTATCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138541  
Oy 1606 ATCTGAATCTCTGAGGCACTGCTGTTGTGCTGCTGTTTCTTAATCTTAATTAATTA 1665  
Db 138540 ATCTGAATCTC-TAGGGCACTGCTGTTGTGCTGCTGTTTCTTAATCTTAATTA 138482  
Oy 1666 CAAATCTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1724  
Db 138481 CAATTTCAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138422  
Oy 1725 AATTGATGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1784  
Db 138421 AATTGATGAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138362  
Oy 1785 GTAAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1841  
Db 138361 GTAAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 138302  
Oy 1842 ACCACTGACCTCTTGG-AGAAAAAGTAATTAATTAATTAATTAATTAATTAATTA 1900  
Db 138301 GCACTGATTTCTCTTGAAGAAAAAAGTAAATGACATTAATCTCTTGAAGATCTTACT 138242  
Oy 1901 TCCCAAAAGTATGAGAAAAAATAATCTCTGTGGCTGGAACAGCTTCTGTTTCTTG 1960  
Db 138241 TCCCAAAAGGATGAGAAAAAAGAAATCTCTTGTGGCTGGAATATCTCTGTTTCTTG 138182  
Oy 1961 CTGCTATATTTGTTAGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2020  
Db 138181 CTGCTATATTTGTTAGCTCTTTAATTAATTAATTAATTAATTAATTAATTAATTA 138122  
Oy 2021 CTAAGTTGAGAGTTTGAATCCCTACAGAGGCACTTCAATTTAGAGAACAAAAAGCCCA 2080  
Db 138121 CTAAGTTGAGAGTTTGAATCCCTACAGAGGCACTTCAATTTAGAGAACAAAAAGCTCT 138062  
Oy 2081 TTCTCTGCTCCAGACCTTACCCCAATCTCTGCCAGGTGTCTGCTCCGCTCAATTA 2140  
Db 138061 TTCTCTGCTCCAGACCTTACCCCAATCTCTGCCAGGTGTCTGCTCCGCTCAATTA 138002

QY 2141 GAACTGCGAAGAGTACTAGAGGTGCGACAGTACTAGAGTGAAGAAAAAGGACTA 2200  
 Db 138001 AGAATTTGGCAAGGGGTGCAAAACATATTCAG----- 137969  
 QY 2201 GCACCTACTAGAGAGCAAGAAAAAGGGACCCCTTCATGAGGTGCTTCCTTCTTCT 2260  
 Db 137968 -----TATGGGAAAAACAAGAGGTGACCCCTTTATCATGATGCTCTTCTTTTAT 137915  
 QY 2261 GTGTTCACATGCTCCGATATATTTTACAGAGGTAGATA-----ACTACATTTT 2312  
 Db 137914 GTGTTCATATATTTCTGATATATTTATAGAGAAATAGATCTGCACCTTTTATCTCTGG 137855  
 QY 2313 TCTTTTACACTGGAAGGCTGAGAAAACTTTGTTACCATCATAAAAATTCATCTTC 2372  
 Db 137854 ATATTTACTGCTGGAAATCTGGGCAAACTGTAAATAGCTCTGCCATCCAGTTATAAAA 137795  
 QY 2373 TAAAGCATTCATGTTATTTCTTAAGATCAATTAAGTACGAGATATCTCTTTGTTAAACA 2432  
 Db 137794 TTCAATTATCTATGTCAGAGATTTTCTACTAGCTGACATTAACCTCTTGGTAAACA 137735  
 QY 2433 ATGAAAAAACAACATCTCTGAGCATATTAATCTGCAACTTATAGATAGAAATCTTA 2492  
 Db 137734 ATG-AAAAACATCTTCTGAGTTATGTTAATCTGCATCTTTAGAAATGAAA-----ATA 137681  
 QY 2493 ATACTAGCAATGAACTGAAATCAATTTTCATATGATAAAGATAT-----TATTT 2547  
 Db 137680 ATAGACTCAGTCAAAAGTTCAGTATATTTTCATATTAATTAAGACATTAATATATGT 137621  
 QY 2548 AAAAGTATTCATAGCAATTTATTAATTA--AAGTAGATTTCTCTTATGTTAAAGAT 2606  
 Db 137620 AAAATATATTCATAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 137561  
 QY 2607 TTATTCAGGGAACAAGTTCTCAATTAATAGCAGAAATCTTTACTAGTACAGCTC 2666  
 Db 137560 TTAGTCA-GAAAAACAAGTTCTCAATTAATAGTAAATTTCTCAACTAGTATCATCTC 137502  
 QY 2667 TTTTCATTTAAGTC-TTCCGTAATTAATCTGATTTTCTAATTAATTAATTAATTAAT 2725  
 Db 137501 TTAATTTTAATTCAGGTCTTCCTTAATTTTATTTTCTTAATTTACTGGCACTAAATA 137442  
 QY 2726 ATTTAATTAATCAAAATTAATTAATTTT--TACTCAAAAGCTTACTTAATTAATTAAT 2784  
 Db 137441 ATTTAATTAATCAAAATTAATTAATTTTCTACTCAAAATCTTGCCTTAATTAATTAAT 137382  
 QY 2785 CATTATTAATTTCTGAGGAAAAAGCATATCACTTTTAAGTATGAGTAAATTAAGAT 2844  
 Db 137381 CATTATTAATTTTGAAGAAATATTTTC-AATTTTAAATATGATATTAATTAATTAAT 137323  
 QY 2845 TTATTCATTAATTAATTAATTTTAAAGTTTCAATTAATTAAGATTAAGATTAAGTG 2904  
 Db 137322 TGACTTATTAATTAATTAATTAAGTGTGAGAGATTAAGATTAAG-----TACAG 137267  
 QY 2905 TATATGTAATGTTAATTAAGTTTATTTTATTTTTCAGTCAATTAAGCCCTTATTAAT 2964  
 Db 137266 TTTATATTAATGCAACATTAAGCTTTGTTTTCAAATGTCACAAATTAATCTTTATTAAT 137207  
 QY 2965 CATAGATTTATTTCTTTTAAGAGTATCAATTAAGTACGCTCACTTGAATGAACA 3024  
 Db 137206 TGTAGATTTATTTCTTTTATAGAGTATCAATTAAGTATGAGCTCACTTGAATGAACA 137147  
 QY 3025 AATACTGTTGGTGACTTGTGACAGACAGGGTTTAACTCTGACAGCGAATTCATGT 3084  
 Db 137146 AATACTGCTGTGTGACTTGTGACAGACAGGGTTTAACTCTGACAGCGAATTCATGT 137087  
 QY 3085 GGAGCAAGAGCAATCAAGATCCGAGACACTGTTCTCATCAAAAGTTGAATTAATAA 3144  
 Db 137086 GGAGCAAGAGCAATCAAGATCCGAGACACTGTTCTCATCAAAAGTTGAATTAATAA 137027  
 QY 3145 AGCACTTGAATACAGTATTAAGATTCACGTGTGTGGCAAGTTGTCTCAAGCTGG 3204  
 Db 137026 AGCACTTGAATACAGTATTAAGATTCACGTGTGTGGCAAGTTGTCTCAAGCTGT 136967

QY 3205 CAGCATTAACCTTTGGCTTGCGCTTACTCAAAAAGCAAAAAGTAAAGAGAACT 3264  
 Db 136966 CATCATTAATTAATTTGCTTGGCATTTACTCAAAAAGCAAAAAGTAAAGAGAAAC 136907  
 QY 3265 AAGAAACAG-GGAAAGATGATTAATTTTAAACCATGCAAAACCTGCAATCTCTGT 3323  
 Db 136906 AAGAAACAGAAAGAAAGATTAATTAATTTTAAATCATGCAAAACCTGCAATCTCTGT 136847  
 QY 3324 TTATATTTACCTTAATTTATGCTGATTTGCTGCGCCAGTGGATGAAATGAGAA 3383  
 Db 136846 TTATATTTACCTGTTATTTATGCTGATTTGCTGCGCCAGTGGATGAAATGAGAA 136787  
 QY 3384 GCAGAA 3389  
 Db 136786 GCAAAA 136781  
 RESULT 12  
 AR211435  
 LOCUS AR211435 3435 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 1 from patent US 6399312.  
 ACCESSION AR211435  
 VERSION AR211435.1 GI:21514756  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 3435)  
 AUTHORS Wu-Mong J.R. and Wang J.  
 TITLE Myostatin gene promoter and inhibition of activation thereof  
 JOURNAL Patent: US 6399312-A 1 04-JUN-2002;  
 FEATURES  
 source 1..3435  
 /organism="Unknown"  
 /mol\_type="unassigned DNA"  
 ORIGIN  
 Query Match 43.0%; Score 1459.2; DB 6; Length 3435;  
 Best Local Similarity 72.7%; Pred. No. 1e-247;  
 Matches 2472; Conservative 0; Mismatches 743; Indels 187; Gaps 38;  
 QY 1 TGCCTGCCGAAGCATAGAGAGTTCGCAATCCCGGCACTGAGAGGAAAGACGCTTC 60  
 Db 119 TTTATTTCTGGGGCTCAGAGAGGTTCATCACTGCACTGAGAGGAAATTAATCTTA 178  
 QY 61 TTGAATTTCTGAGTACTCTTATTCATTAATGCTGACCTCGGA-----GATTGG 114  
 Db 179 CTTAAATTTCTTCAAGTTCTTCTTCAACCATTAATCTGTTCTTAAAGAAATGATTAAG 238  
 QY 115 ATAGAGTGACTCTCATTAATTTACAGAGTGTATGTTTACCCAAATCACTGCCAACA-TGA 173  
 Db 239 ATATAGTCAATTTCTCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 298  
 QY 174 ATATAGTATTCCTGAACCACTGCGCCCTAGAGGAACTCAAGGTAAATTTCCCGACCT 233  
 Db 299 GTTAGCAAAATTAATTAATTAATTTGTTCCAGAGGAAAGAAAGAGTTGAGGCTCTG-- 355  
 QY 234 CTGTGACAGTTTGTATTAACCAATCAATTAATTAATTTGTTGTCATTTCTGTTT 293  
 Db 356 GTCAATTAATTAATCAACCAATCAATTAATTAATTAATTTGTTTATGATTTTGTTTA 415  
 QY 294 AAAATATCTTTATTAATTAATTAATTAATTTCTTCAACATTTGTTTCAACCAAAAG 353  
 Db 416 CAATTA-CATTAATTAATTAATTAATTAATTTGTTCAATTAATTAATTAATTAATTA 470  
 QY 354 CCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCTATGAGA 413  
 Db 471 CAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCTATGAG 527  
 QY 414 AAAATTTTCTTCAAGCTGCGCAAGCTTTCTGTTAAATTTGGAAGAAATTAATTA 473  
 Db 528 AACTTTTCTTCAAGCTGCGCAAGCTTTCTGTTAAATTTGGAAGAAATTAATTAATTA 582

474 TAACTGAACTGACTATTTATTTAACTGATTTTAACTGATGCTGAGTCATTAAGTA 533  
583 ACATTTAGCA-----TCTTAACCAATTTTATAGGTGATGAGTTGCGGATTAAGCA 633  
534 CACTTACTGCTGTGGAACCTATGATCAACATTTCTCTGAACTTTTGTATCTTCTCG 593  
634 CATTCACTGTGTGTAAACCATCAACACATTCATCTTCAGAAAATTTTCAATCTTCCA 693  
594 AATTGAAACTCTGATCTATTTGACAGTAGCTTTTCCCATCAGACCGACCTTCTCTC 653  
694 GACTG-AAACTCTGTATCTATCAACAGTAATCTACCTCTCA-----GTGCTTACG 743  
554 CAGCCCCCGGACCAACCATCTTCTTTCATGACAGTCATCTGTGCTTGAAGCA--- 710  
744 CAGTCCCTGGCAACCAACCATGCTACTTTCATTTGACGCTTCTGTGATTTAGAACAT 803  
711 -----CAGCCTTCAACATGACTGCTTGGGGGCACTGT---AAGCAACGATC 756  
804 GAACACACGACGACGTCAGCATGCTTGGGGGCCATTTTAAAAAGCAAAATCAT 863  
757 ACTCCCTACCGCACCAATGACACAAAATATATAAAGCATGCTGGCATTCGATTCG 816  
864 AAGAGACATTAATAAAGAAAGCAAAATATGTAAACATGSCATTAATTAAGCGG 923  
817 AAAAAAGGTGCTGCT--AAGTAGAGGGCTGAAAC---AAGCAGAGATTTAGTAGT 871  
924 AAAAAAGGAATTTGTTATAGTATGAGAGCTGAACAAAAGCGGAACCTGCTTGT 983  
872 TGACTCAGCTGGATCTCTGTGTGG--AAGCTCAAAATTTTCATTTCTGTGAT 929  
984 TGACTCCTGCGGAACCTGTGCGTCAGATAGACTCAAAATTTTTCGCTGTGTGAT 1043  
930 ACGCAAAATGCTTATAAAGCACTGTAAAGATGATTAAGTTAAGTTAATCTCG 989  
1044 GCCACGAATGACTAAAA---TGTAGGAATTTGAGTTTCAATGATTAATTTTAC 1099  
990 CAAGCATTAATGTGCAAGCAGGAGTCATGATTAAGCAGCATGACAT--GTGAAA 1047  
1100 AAGTAGCAAAATTTGTGAATACAGAAATCATGATTAATGAATTTGTCTTGAAGGAAA 1159  
1048 TGATTAATTTTGTCTTCTTATTTCAAGGAGTAAGAGAAAGCG-----T 1093  
1160 TGACAACTTTGTTCATCTTTTCCAGGTGATTAAGATTAAGAGCTGAAACATGTCTTGT 1219  
1094 CACAGGGCTGCTTACACCATTTTCTAGAGAGCTAGCTTATGTGAGTGG----- 1144  
1220 AACCTGGCTGCTTGAATAATTTTACTGTCTCAGAGCTTGAAGAGAGGCTTTGTGAC 1279  
1145 ---TAGTGGCAATTACAACAGTGAAGAGTTCTAGTTCATGTGAGATGATTTAACA 1201  
1280 TGATTAATGGGAGCTATGACCTGAAGAGTTCTAGTTCATGTGAGCATTAATTTAACA 1339  
1202 TAATTTCAACCCCTCTGTGATGAACAGAGACTAAGTACTCAAGTACAGATTATAGTCA 1261  
1340 TAATCTCAACCTTCTGCATTAACAAAGAGCAAGCACTCAAAAGCCAGTTATCAATTA 1399  
1262 CTACTATATGACAGGACCTGACTCAACAAATTTTACATGATTAATTTAATGATGACC 1321  
1400 CTACTATATGACAGGTCATATTTCAAGCAATTTTACAGCATTAATTAATATATCCCC 1459  
1322 CAACACTATGAGAGCTGAAGGTTAG---AAGTATCTCATTTATTTATACCA 1376  
1460 CAAAACCTATGAGAGCTAAAGTTTAGGAAAGTTAAGTATCTATCATTTATACATA 1519  
1377 GT-----GGCAACTGAGATCTGAATCTGATTCACATCTCAGACCTGAGATC 1428  
1520 GTTAGAGGTGGCAAGTTGAGATTTGAACCTGAGTCTATCTGACCTCCAGAGCTGAGTTC 1579  
1429 CCAATTGTACACATTTGATTAATCAAGTTAAAGGAAAAAGGATTTGATTTGCTGAGAG 1488  
1580 TCAATTCAACTGCTATACATTTCTAAGCATTAATAAAGAAAGTTGACTTACCTGGAAC 1639  
1489 TGTATAGGGCATATGTTACA---ATTATTAATTACAAGATTTATATGTTGAATAATA 1545

1640 TGTATAGATGATGTGTACATGATCATTAACATTTGAAAGATTTACATTTGAAAAATG 1699  
1546 AATTATCAACAAATTAATCTTTAATAGCCGTATCTAATCTGCTCGCAACAAAGCT 1605  
1700 AATTATCAACAAATTAATCTTTAATAGCCGTATCTAATCTGCTCGCAACAAAGCT 1759  
1606 AATCGAAATCTCTGAGGCACTGTGTTGTCTGTGTTTCTTAATCTTAATGATGG 1665  
1760 ATCTGAATCC--TCAAGGCACTGTGTTGTGTCTGTGTTTCTTAATCTTAATGATGAG 1818  
1666 CAATCTAATSCATTAATGTAAGGCCA--TTTTTCTCAAGAGATGATATCTCTTAAGA 1724  
1819 CAAATCCATGATATGTAAGGCCATTTTCTCAAGAGATGATATCTCTTAAGA 1878  
1725 AATTGTAAGAAATGATTAATCTTTTCAAGGCTACGATGATGATTTGATGACAGGCA 1784  
1879 AATTGATGAATGATATTAATCTTTTCAAGGCTACGATGATGATTTGATGACAGGCA 1938  
1785 GTAAATTAATGATGATGTAAGGCCA---GTAGTACCTTAATAAATTAATTTGATATGA 1841  
1939 GTAAATTAATGATGATGTAAGGCCA---GTAGTACCTTAATAAATTAATTTGATATGA 1998  
1842 ACCACTGACTCTCTTGG--GAAAAAAGTAATGATTAATCTCTTACGAGTCTTACCT 1900  
1999 GCCACTGATTTCTCTTGGAAAAAAGTAATGATGATTAATCTCTTACGAGTCTTACCT 2058  
1901 TCCCAAAAGTAATGTAAGAAATTAATCTCTGTCGCTGGAACACGTTCTGTTCTTG 1960  
2059 TCCCAAAAGTAATGTAAGAAATTAATCTCTGTCGCTGGAACACGTTCTGTTCTTG 2118  
1961 CTGCTATATTTGTTAGTTTATTAATGATTAATCTCTGTCGCTGGAACACGTTCTGTTCTTG 2020  
2119 CTGCTATATTTGTTAGTTTATTAATGATTAATCTCTGTCGCTGGAACACGTTCTGTTCTTG 2178  
2021 CTAAAGTTGAGATTTGATTCCTTACAGAGGCACTTCAATTTAAGAACAAAAAGCCCA 2080  
2179 CTAAAGTTGAGATTTGATTCCTTACAGAGGCACTTCAATTTAAGAACAAAAAGCCCA 2238  
2081 TTTCTGTCTCCCAACCTTACCCCAATCCCTGCAAGTGTCTGCTCGCTGCAAAATGA 2140  
2239 TTTCTGTCTCCCAACCTTACCCCAATCCCTGCAAGTGTCTGCTCGCTGCAAAATGA 2298  
2141 GAACTGGCAAGGAAGTACTAGAGAGTCCGACAGTACTAGAAATGAAATGACCTA 2200  
2239 AGAATTTGGCAAGGGGTGCAAC-----TA 2325  
2201 GCACACTATGAGAAAGCAAAAAATGGGACCTTCATGATGTGTCTTCCCTTCT 2260  
2326 TCGAGATTTGGAAACAAACAAAGGTCAACCTTTATCATGATGTCTTCTCTTTAT 2385  
2261 GTTCTCAATATGCTCCCATTAATTAATTTACAGAGGTAATA-----ACTACATTTT 2312  
2386 GTGCTCATTAATTTCTGATTAATTTATTAAGAAATGATGTGCACTTTTATCTCTGG 2445  
2313 TCTTTACCACTGGAAGCTGAGAAAACTTGTGTAACCATCATTAATTTACATCTTC 2372  
2446 ATATTTACTGTGGAATCTGAGCAAACTTAATATCTGTGCAATGCCAGTTATAAA 2505  
2373 TAACTGATTTCTATGTTATTTAAG-----TCAATATGCTGACAAATATCTCTTTGTA 2426  
2506 TTCAATTTACTGATGTTATGTTCAAGATTTTCTACTAGCTGAGATTCCTCTTGTA 2565  
2427 TAAACATGAAAAACACATCTCTGAGCAATATTAATCTGCACTTTAGATAGAGT 2486  
2566 TAAACAAAG--AAAAACATCTTCTGAGTTATGTTAATCTGCACTTTTGAATGGA-- 2622  
2487 AACTTAATACTAGTCAATTTGAAGTGAATCAATTTTCAATGATTAATTAAGAT-- 2542  
2623 ---ATAATGACCTGACCAAGTTGATTAATTTTCAATTAATTAAGACATGAAA 2679  
2543 -TAATTAAGTAAATTCATGAGCAATTAATTAATTA--AAGTAGATTTTCAATATGTGT 2600





|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| QY | 990  | AAAGACATTAATGTCAGACAGGGATCTAGAAATTAACGACACTGCACAT--GTGGAAA     | 1047 |
| Db | 1100 | AAGTAGGCAAAATTTGTGATACAGAAATCATGAATTAATAAATTTGTCTGTACGGAAA     | 1159 |
| QY | 1048 | TGATTAATCTTGTGTTCTCTTAATTCAGGACGATAAGAGAAAGCC-----T            | 1093 |
| Db | 1160 | TGACAACTTTGTTCACTTTTTCCAGGTGATTAAGAAATTAAGACGTGGAACTCTTGT      | 1219 |
| QY | 1094 | CACAGGGCTGCTTAACACCATTTTACTAGAGCTAGCTATGTCAGTGG-----           | 1144 |
| Db | 1220 | AACCTGGCTGCTTAGAAAATTTTACTTGCCCTCACAGGCTTAGAAAGTAGAGCTTTGTGAC  | 1279 |
| QY | 1145 | ---TAGCTGGCAATTAACAACGTGAAGAGCTCTAGTTCAATGTGAGATGAAATTAACA     | 1201 |
| Db | 1280 | TGATTAATTTGGAGCTATGACCTGAAGAGCTTCTAGTTCAATGTGAGAGCTAATTTTAAGA  | 1339 |
| QY | 1202 | TAACTCAACCCCTCTGCTGATGAACAGAGACTAAGTACTCAAGTACCAAGTTTCACTCA    | 1261 |
| Db | 1340 | TAACTCAACCCCTTCTGCTATTAACAAAGAGCAAGCACTCAATGCGAGTTATCAATTA     | 1399 |
| QY | 1262 | CTTACTATATGACAGGCACTGTACTCAACAATTTACATGATTAATGAATTAACATGCCCC   | 1321 |
| Db | 1400 | CTTACTATATGACAGGTGCTCAATTTACAGCAATTTACATGACATTTAATAATTAATCCCC  | 1459 |
| QY | 1322 | CAACACTCTATGAGGAAGCTGAAGTTAG-----AAGTATCTCATTTATTAACA          | 1376 |
| Db | 1460 | CAAAACCTTAAGAGAAAGCTAAAGTTTAAAGGAAGTTAAGTCTCATCTCATTAATCACTA   | 1519 |
| QY | 1377 | GT-----GGCAAACTGAGATGCTGAAGCTGATCCATCCAGACCTGAGATC             | 1428 |
| Db | 1520 | GTTAGAAGTGGCAAAAGTTGAGATTTGAATCAAGGTCTATCTGACTCCAGAGCTGAGTTC   | 1579 |
| QY | 1429 | CCAAATTGCTACACAATTTCTAATCAAGTTAAAGGAAAAAGAGATTTGCTCAGAG        | 1488 |
| Db | 1580 | TCAATTAACACTGCTATACAAATTTCAAGCATTTAABAAAAAAGTTGACTTACTTGAAAC   | 1639 |
| QY | 1489 | TGTTATGGGGCAATATGTTACA---ATTATACTTACAAAGATTTATATGTTGAAAAATA    | 1545 |
| Db | 1640 | TGTTATAGATGATGTGTTACATGATGCTAAACATTTGAAABAATTTACATTTGAAAAATG   | 1699 |
| QY | 1546 | AATTATCAAAACAATAAACCCTTAATAAGCTGATCTAATCTGCTCGGCAACAAGACT      | 1605 |
| Db | 1700 | AATTTTACAAACAANTTAACCTTAAGAGCGAGATCTAATATTTGTCCTATACAAAGAGT    | 1759 |
| QY | 1606 | ATCTGAATCCTTCAGGGCATCTGTTGTGTCTGCTTTTCTTAATCTTTAATGATGGG       | 1665 |
| Db | 1760 | ATCTGAATTC--TGAGGCACTGTGTTGTGTCTGCTTTCTTAATCTTTAATGATGAG       | 1818 |
| QY | 1666 | CAAACTTAATGCAATTAATTAAGGCA--TTTTTCTCAAGAGATGATACCTCTTAAGA      | 1724 |
| Db | 1819 | CAAACTCAATGCAATTAATTAAGGCCAATTTTTTCTCAAGAGATGATACCTCTTAAGA     | 1878 |
| QY | 1725 | ATTGATGAAGAATGATTAACCTTTCAAGGCTACGATGTCGATTTTAATGACAGGCA       | 1784 |
| Db | 1879 | ATTGATGAAGAATGATTAACCTTTCAAGGCTACGATGTCGATTTTAATGACAGGCA       | 1938 |
| QY | 1785 | GTAATATTGTTACAAATGTCGAAA---GTAGTGCCTAAAAAATAATTAATTTGATATGA    | 1841 |
| Db | 1939 | GTAATATTGTTACAAATGTCGAAAATGTTGATGACTTTAATAAATAATTAATTTGATATGA  | 1998 |
| QY | 1842 | ACGACTGACCTCTCTGG--GGAAAAAGTAATGATTAACCTCTTAGAGTCTTACT         | 1900 |
| Db | 1999 | GCGACTGATTTCTCTTGAAAAAAAATAATTAATGACCTAATCTCTTAGAATCTTACT      | 2058 |
| QY | 1901 | TCCCCAAAGATAGTGAAGAAAAATAATCTCTCTGTGGCTGGAAAAAGCTTCTGTTTCTTG   | 1960 |
| Db | 2059 | TCCCCAAAGATAGTGAAGAAAAATAATCTCTCTGTGGCTGAAGAAATATCTTCTGTTTCTTG | 2118 |
| QY | 1961 | CTGGCTATATTGTTAGTTTATAGTTTATAGTTTATAGACTTGTGCTCCCAAG           | 2020 |
| Db | 2119 | CTGGCTATATTGTTAGTTTATAGTTTATAGTTTATAGACTTGTGCTCCCAAG           | 2178 |
| QY | 2021 | CTAAGGTTGAGATTGATCCCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCCCCA     | 2080 |

[illegible]

Db 3214 CATTGTGAGCAGACGCCAATCATATGATCTGACGACACTTGTCTCATCTAAGTTGGAA 3273  
Qy 3139 ATAAAAAGCCACTTGGAAATAGATATAAAAGTTCACTGTGTGGCAAGTTGTCTCTAG 3198  
Db 3274 ATAAAGCCACTTGGAAATAGATATAAAAGTTCACTGTGTGGCAAGTTGTCTCTAG 3333  
Qy 3199 ACTGGGCGGCACTTAACTTGGCTTGGCTTGGCTTAAAGCAAAAGAAAGTAAAGGA 3258  
Db 3334 ACTGTACATGATTAATTTTGTGGCTTGGCTTAAAGCAAAAGAAAGTAAAGGA 3393  
Qy 3259 AGAGTAGACAGACGAGAAAGATTGTATGATTTTAAACC 3300  
Db 3394 AGAAACAGAACAGAAAGATTATATTTTAAATC 3435

RESULT 14  
BTA438578  
LOCUS BTA438578 1269 bp DNA linear MAM 08-APR-2002  
DEFINITION Bos taurus partial gdf-8 for myostatin and promoter region.  
ACCESSION AJ438578.1 GI:20135841  
VERSION gdf-8; myostatin.  
KEYWORDS Bos taurus (cow)  
SOURCE Bos taurus  
ORGANISM Bos taurus; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1  
AUTHORS Crisa, A., Marchitelli, C., Savarese, M. and Valentini, A.  
TITLE Sequence analysis of the myostatin promoter region in cattle  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1269)  
AUTHORS Crisa, A.  
TITLE Direct Submission  
JOURNAL Submitted (08-MAR-2002) Crisa A., Produzioni Animali, Università degli Studi della Tuscia, Via S. Camillo de Lellis s.n.c. 01100 Viterbo, ITALY  
FEATURES  
SOURCE Location/Qualifiers  
1..1269  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
gene complement(237..242)  
/gene="gdf-8"  
enhancer complement(237..242)  
/gene="gdf-8"  
1008..1269  
gene /gene="gdf-8"  
CAAT\_signal 1008..1011  
TATA\_signal /gene="gdf-8"  
1051..1057  
TATA\_signal /gene="gdf-8"  
1075..1081  
CDS /gene="gdf-8"  
1214..>1269  
/gene="gdf-8"  
/codon\_start=1  
/product="myostatin"  
/protein\_id="CAD27441.1"  
/db\_xref="GI:20135842"  
/db\_xref="Uniprot/TREMBL:Q8SPM3"  
/translation="MQKQISVLYLFLMLIVAG"

ORIGIN  
Query Match 36.9%; Score 1251.2; DB 4; Length 1269;  
Best Local Similarity 99.5%; Pred. No. 6.2e-211;  
Matches 1264; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

Qy 2087 GCTCCAGACCTTACCCCAATCCCTGCGAGGTGTCTGCTCCGTCGAATGAGAAGT 2146  
Db 1 GCTCCAGACCTTACCCCAATCCCTGCGAGGTGTCTGCTCCGTCGAATGAGAAGT 59  
Qy 2147 GGCAGAGAGAGTACTAGAGGTGCGACAGTACTAGAAAGTAAAGTGAAGTGAAGT 2206

Db 60 GGCAAGAGAGTACTAGAGGTGCGACAGTACTAGAAAGTAAAGTGAAGTGAAGTGAAGT 119  
Qy 2207 TACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2266  
Db 120 TACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 179  
Qy 2267 ACAATGCTCCGATTAATTTTACAGAGGGTGAATTAATTAATTTTCTTTTACACATGG 2326  
Db 180 ACAATGCTCCGATTAATTTTACAGAGGGTGAATTAATTAATTTTCTTTTACACATGG 239  
Qy 2327 AAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2386  
Db 240 AAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 299  
Qy 2387 TTATTTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAAT 2446  
Db 300 TTATTTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAAT 359  
Qy 2447 CCTCTGAGCAATTAATTAATTCGCAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2506  
Db 360 CCTCTGAGCAATTAATTAATTCGCAACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 419  
Qy 2507 AAATGAAATCAATTTTCAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2566  
Db 420 AAATGAAATCAATTTTCAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 479  
Qy 2567 ATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2626  
Db 480 ATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 539  
Qy 2627 CTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2686  
Db 540 CTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 599  
Qy 2687 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2746  
Db 600 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 659  
Qy 2747 TATTTTACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2806  
Db 660 TATTTTACTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 719  
Qy 2807 GCATATCACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2866  
Db 720 GCATATCACTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 779  
Qy 2867 TTAAGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2926  
Db 780 TTAAGTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 839  
Qy 2927 TTTTAAATTTTGGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2986  
Db 840 TTTTAAATTTTGGAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 899  
Qy 2987 AGTAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3046  
Db 900 AGTAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 959  
Qy 3047 CAGACAGGGTTTAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3106  
Db 960 CAGACAGGGTTTAACTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019  
Qy 3107 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3166  
Db 1020 CCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1079  
Qy 3167 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3226  
Db 1080 AAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1139  
Qy 3227 CTTTACTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3286

```

Db      1140 CGTACTCAAAAGCAAGAAAGTAAAGAGAGAGTAAAGACAGGAAAGATTGTA 1199
Qy      3287 TTGATTTTAAACATGCAAAAGTGCAGAACTCTGTTTATTATTACATTATTATGCGA 3346
Db      1200 TTGATTTTAAACATGCAAAAGTGCAGAACTCTGTTTATTATTACATTATTATGCTGA 1259
Qy      3347 TTGTTGCTGG 3356
Db      1260 TTGTTGCTGG 1269

RESULT 15
AC140969/c
LOCUS   AC140969
DEFINITION  Canis familiaris clone RP81-197A18, WORKING DRAFT SEQUENCE, 11
ordered pieces.
AC140969
VERSION 1
KEYWORDS HTG; HTGS PHASE2; HTGS_DRAFT.
SOURCE   Canis familiaris (dog)
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Canidae; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS 1 (bases 1 to 192219)
          Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
          Blakeley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Carlsaga,K.,
          Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X.,
          Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P.,
          Hurler,B., Idol,J.R., Karling,E., Kwong,P., Latic,P., Lee-Lin,S.-Q.,
          Legaesi,R., Maduro,Q.T., Maduro,V.B., Margulies,E.H., Mastello,C.,
          Maskei,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E.,
          Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K.,
          Sison,C., Stancirpop,S., Thomas,J.W., Thomas,P.J., Tidipuri,V.,
          Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
          NISC Comparative Sequencing Initiative
          Unpublished
          2 (bases 1 to 192219)
          Green,E.D.
          Direct Submission
          Submitted (06-MAR-2003) NIH Intramural Sequencing Center, 8717
          Grovemont Circle, Gaithersburg, MD 20877, USA
          3 (bases 1 to 192219)
          Green,E.D.
          Direct Submission
          Submitted (16-MAY-2003) NIH Intramural Sequencing Center, 8717
          Grovemont Circle, Gaithersburg, MD 20877, USA
          On May 16, 2003 this sequence version replaced gi:28867001.
          ----- Genome Center
          Center: NIH Intramural Sequencing Center
          Center code: NISC
          Web site: http://www.nisc.nih.gov
          Contact: nisc_zoo@nhgri.nih.gov
          ----- Project Information
          Center project name: eaj
          Center clone name: 197A18

```

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics -----  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 190062 bases at least Q40

```

FEATURES
source
1..192219
location:Qualifiers
  /organism="Canis familiaris"
  /mol_type="genomic DNA"
  /db_xref="taxon:9615"
  /clone="RP81-197A18"
  /clone_1fb="RP81"
  1..1927
  /note="assembly_fragment"
  clone_end:17
  vector_side:left"
  2028..88251
  /note="assembly_fragment"
  88352..107063
  /note="assembly_fragment"
  107164..109235
  /note="assembly_fragment"
  109336..119132
  /note="assembly_fragment"
  119233..192219
  /note="clone overlaps with GenBank Accession Number AC140667 clone RP81-292C20 (center project name eak)"
  119233..125483
  /note="assembly_fragment"
  125484..140954
  /note="assembly_fragment"
  141055..143181
  /note="assembly_fragment"
  143282..158769
  /note="assembly_fragment"
  158870..163950
  /note="assembly_fragment"
  163950..192219
  /note="assembly_fragment"
  clone_end:SP6
  vector_side:right"

```

Consensus quality: 190807 bases at least Q30  
Consensus quality: 191127 bases at least Q20  
Insert size: 172000; agarose-fp  
Insert size: 191219; sum-of-contigs  
Quality coverage: 10.69x in Q20 bases; agarose-fp  
Quality coverage: 9.61x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 1927: contig of 1927 bp in length  
1928 2027: gap of unknown length  
2028 88251: contig of 86224 bp in length  
88252 88351: gap of unknown length  
88352 107063: contig of 18712 bp in length  
107064 107163: gap of unknown length  
107164 109235: contig of 2072 bp in length  
109236 109335: gap of unknown length  
109336 119132: contig of 9797 bp in length  
119133 119232: gap of unknown length  
119233 125483: contig of 6251 bp in length  
125484 125583: gap of unknown length  
125584 140954: contig of 15371 bp in length  
140955 141054: gap of unknown length  
141055 143181: contig of 2127 bp in length  
143182 143281: gap of unknown length  
143282 158769: contig of 15488 bp in length  
158770 158869: gap of unknown length  
158870 163949: contig of 4980 bp in length  
163950 163949: gap of unknown length  
163950 192219: contig of 28270 bp in length.

## ORIGIN

Query Match 32.1%; Score 1088.6; DB 2; Length 192219;  
Best Local Similarity 67.3%; Pred.No.1.5e-182;  
Matches 2222; Conservative 0; Mismatches 694; Indels 387; Gaps 33;

QY 451 TAAATGTTGACAAAATATCATPAACATGAACGACTATATTTATTTAACT 510  
DB 92723 TAAAACTCCAGTAAACATATPAACATTAATTTGAC--CACTGAACCAATTTTAAGT 92667

QY 511 GTACAGTTCACTGACATTAAGTATACACTTACCTGCTGGAACATATGATCAACATTC 570  
DB 92666 GTACATTTCACTGACATTAAGTATACACTTACCTGCTGGAACATATGATCAACATTC 92608

QY 571 TCTGAACCTTTTGAATCTTCTGCAATGAATACTCTGCAATTAATGACAGTACCTTCC 630  
DB 92607 TCCGAACCTTTCTATCTTCCCAATG--AACTCTGATCCTGCTGAATGAACCTCCGC 92549

QY 631 CCCATCAACGACACCTTCTCCAGCCCCCGGACACCATCTTCTTCCATGACAG 690  
DB 92548 CCCCCCCCCCAACCCCTGCTCAAAATCCCTGGCAACCACTTCTTCTTCAACAG 92489

QY 691 TCATCTGTGCTGCTGGAACACAGCCCTTCAACACTACGCTTGGGGGCACTGTAAAGAC 750  
DB 92488 CTTCTTTTATTAAGGACAGACACTTACCTCTATGCTTACGCTTGAAGCACTTTAAATG 92429

QY 751 AGGATCACTCCCTACCCGACCAATGACCAAAATATA--AAAGATGCTGAT 807  
DB 92428 AATGCCCCAGAAAGGCTTACCAATCAAAAAATTAATAAACCCACTTGGTAA 92369

QY 808 ATGATGCAAAAAGGGGCTTGTCT--AAGTATAGGCTGAAACAAAGGCAAGAAATGA 865  
DB 92368 ATATATGTAAGAAAGGCACTTGTTCACAGATAGAGCTGAACAAAGTGAACGTTGC 92309

QY 866 CTAGCTGACCTCACTGAGATCCCTGCTGTTGAAGGCTCAATTTTCCATTTCTGT 925  
DB 92308 CT-TGTTGACCTGGCTAGAGGCTGTGTGTTGAAGTTCAATTTTTCACAGCTGC 92250

QY 926 GCATACGCAAAATGCTTATAAAGCACTGAAGATTAATTAAGAAATGA 983  
DB 92249 GCGGTGCACAGTGAACCAAAATCAATCTGATTAATTTGGGGTTTAAATTAAT 92190

QY 984 TCTCAGAGACATTAATGTCAGACGCGGATCATGAATTAAGAGACAGAC--CATG 1041  
DB 92189 TTTAGCAAGAGGCGAATTTGAAGATGAAATTCATCAATTAAGAACATCACTGTATG 92130

QY 1042 TGGAAATGATATCTTTTCTTTTCTTTATTCAGGACAGTAAAGAAAGCGCT--CACAG 1099  
DB 92129 TGGAAATGGAACCTTTGTTTACGTTATTCAGTAAAGTAAAGAGCTGAATAATG 92070

QY 1100 GCTGCTTACACATTTTCTAGAGAGCTGATGTCAGTCCGTAGCTGGCAATTA 1159  
DB 92069 CTTATCATGAGGCTCTTGAAGAAATTTTGTCTGTGATTAATCTGGCAGTACA 92010

QY 1160 AACTGAAGAGCTTATGATCAATGAGAGATTAATTAACATTAATCAACCCCTCTG 1219  
DB 92009 AACTGAAGAGCTTATGATGCTGTGGAGAGATTAATTAAGATATATCAAAACCCCTCTG 91950

QY 1220 CATGAAACAGAGCTAAGTACTCAAGTACAGTATCACTCACTTATTAATGACAGCA 1279  
DB 91949 CA-GGAACAAAGACTGAGACTCAAGTAACTATCATCACTTACTGTAAGACAGCA 91891

QY 1280 CTGATCTCAACATTTATCATGATTAATTAATTAATTAATTAATTAATTAATTAATTA 1339  
DB 91890 CTATATTCAGCATTTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 91831

QY 1340 CTGAAGTTAGAGAGT-----ATCTCATCATTAATTAACAG-----TGGCAACT 1386  
DB 91830 CTGAAGTTAGAGAGTTAAAGACCTATCGTTATCACTGATCAAGTGAAGTGAACATTT 91771

QY 1387 GAGATCTGAACCTCACTCATCAACTCAGAGCTGAGATCCCAATTTGCTACCAATTC 1446  
DB 91770 GAGATCTGAACCTCACTCGTGGAGCTCCAGAGCTGAGTCCCACTGCTATGCAATTC 91711

QY 1447 TAATCAAGTTAAAGGAAAGAGATTTGATTTGCTCAGAGTGTATAGGGCATATGTT 1506  
DB 91710 TAATCAAGATTCAAAAAAG--TCCAATCTACTCAGAGTGTATAGGACATATGTT 91653

QY 1507 ACA---ATTATPACATTAACAAAGATTTATGTTGAAATAATTAATTAATTAATTAATTA 1563  
DB 91652 ACATGATTAATGATGCGCAAGACTTATACAGAGAAATTAAGCTT---ACCAATTA 91597

QY 1564 AACTTATTAAGCTGATCTAATCTGCTCCGCAACAAGACTATCTGAAATCTTCCAGG 1623  
DB 91596 AACTTATTAAGCTGATCTAATGTTGTTCCAAATAAAGATATCTGAATCTTCCAGG 91537

QY 1624 CATCTGTTGTGTCTGTTTCTTATCTTTAATGATGGCAATCTAATGATTAATG 1683  
DB 91536 AATCTGTTGTGTCTGTTTCTTATCTTTAATGATGAGCAAACTAATGATTAACG 91477

QY 1684 TAAAGCC-----ATTTTCTCAAGAGATGATPACCTTAAGAAATTTGATGAAT 1737  
DB 91476 TAAAGCCGTTTCTTCTCAAGAGATGATPACCTTAAGAAATTTGATGAAT 91417

QY 1738 GCATTAATCTTTTCAAGCTACTGATGTTGATTTAGTCACTGAGGAGTAAATTAATGTA 1797  
DB 91416 GCATTAATCTTTTCAAGCTACTGATGTTGATTTAGTCACTGAGGAGTAAATTAATGTA 91357

QY 1798 CAATGTCGAAA--GTAGTACCTTAATAATAATTAATTAATTAATTAATTAATTAATTA 1854  
DB 91356 CAATGTCGAAAAGGTGATGACCTAATAATAATTAATTAATTAATTAATTAATTAATTA 91297

QY 1855 CTT-----GGGAAAAAAGTAAAGATTAATCTCTTAAGAGTCTTAAGCTCCCA 1906  
DB 91296 GTTGGGGTGAAGGGCTCAAGTAAAGATTAATCTCTTAAGAGTCTTAAGCTCCCA 91237

QY 1907 AAAGTATGAGAAAAATTAATCTCTGCTGCTGGAACAGCTTCTGTTCTTCTGCT 1966  
DB 91236 AAAGTATGAGAAAAAATTAATCTCTGCTGCTGGAACAGCTTCTGCTGCTGCT 91179

QY 1967 ATATTTGTTTATGTTTATTAATGTTCAATTTGATTAAGCTTGTGCTCCCAAGCTAAG 2026  
DB 91178 GTTGTGCTTATGCTTATTAACAGTTTATTAAGTAAAGTCTCTGCTCCCAAGCTAAG 91119

QY 2027 TTGAGATTTGATCCCTACAGAGAGCACTTCAATTTAAGAAACAAAGGCCCATCTCT 2086  
DB 91118 TTGAGATTTGATCCCTACAGAGCACTTCAATTTAAGAAACAAAGGCCCATCTCTCT 91059

QY 2087 GCTCCAGACCTTACCCCAATCTCTGCAAGTGTCTGCTCCCTGCTC--AAATGAGAAAC 2145  
DB 91058 GCTCCAGACCTTACCCCAATCTCTGCAAGTGTCTGCTCCCTGCTC--AAATGAGAAAC 90999

QY 2146 TGGCAAGAAAGTATGAGAGT----- 2168  
DB 90998 TGGCAAGAGGCTCAACAGTATTAATTTGGGGGACCAACAAATGGGCAACCCCTTAT 90939

QY 2169 -----CGACAGTACTGAAGTGAAGAAATGAGCTAGAC 2204  
DB 90938 AGGCTGCTCTTCACTCTTAAGTGTCTACAGTATTTGATTAATTAATTAATTAATTA 90879

QY 2205 ACTACTGAGAGAGAG----- 2220  
DB 90878 GCGCTGAGGAGGCTCAAGTGTCTGCTTGGCTCAAGTGTGATCTCAGG 90819

QY 2221 -----AAATGGGCAACCTTCAATGATGTTCTTCTTCTT 2257  
DB 90818 GTTCAAGGATCCAGAGTGAAGCCCAATGAGGCTCCCTGCTCAGCGGGAGCTGTGCTT 90759

QY 2258 TCTGTGTTCAATGCTCGAT----- 2279  
DB 90758 CTTCTTCTGCTGCTCCCTTCTGCTGCTGCTCTCTCTCAATTAAGCAAT 90699

QY 2280 ----- 2279  
DB 90698 AATCTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 90639

QY 2280 -----ATGA 2283  
Db 90638 AAAATAAGGCTTTCTGATTTCTCAAAATAGAAATGATCCTTAAAAATAATAATTA 90579  
QY 2284 TTTACAGAGGTAATACATATTTTCTTTACACCTGGAAGCTGAGAAACTT 2343  
Db 90578 CTTATGAGAGAGAT-ACATAGCTTTTCTTTTACCTGTAGAAATCTGAGGCAAGTG 90520  
QY 2344 T-----GTACCATCATAAATTCATCTTCTTAACTCATTTATTT 2391  
Db 90519 TAGCAAGTGCAGCATTTGTACGTATACAGTTACTTTAT-TCATAGTTGAGGTTT 90461  
QY 2392 CTAAAGTCAATAGCTGACATATCTCTTTGTAATAACATGAAAAACATCTCT 2451  
Db 90460 TTTTCTCTGATGATACATTTAGCTCTTGTAATAACATGAAAAACATCTCT 90401  
QY 2452 GAGCAATTTATCTGCACTTTAGATAGGAAGTAATTAATCTAGTCAATGAACT 2511  
Db 90400 GAGTAATTTTAACTGCACTTCAAAATAGAAATTAAGTAATGCAATCAGCCAAAAG 90341  
QY 2512 GAAATCAATTTTCAATGATATAA-----GATATATTTTAAAGTAATTCATGACA 2566  
Db 90340 TGAGCAGAGTTTCAATTTATATAAACAATGAAATTTTCAAAAGATTTCCATGTGA 90281  
QY 2567 ATTTAATAT- -AAAGTAGATTTTCAATTAATGTAGATTTTCAAGGAAACAG 2623  
Db 90280 ATGAAACATTTGTAAGAGTTGATTTTAGATGTAGATTTTAAATCAGAAACAG 90221  
QY 2624 TTTCTCAATTTATGCAAAATTTTCTAGTATCA-----GTCTTTTCAAT 2673  
Db 90220 TTTCTCAGATTTATAGCTGAAATCTTTTACTAGTACATGTCACTTTTATTTTAT 90161  
QY 2674 TTAAGTCTCTGAT- -AAATCTGATTTTCTAATTTATCAAGCTAAAAATTAATTA 2731  
Db 90160 TCAGGTTCTCTTATTTCAATTTCAAGTCTCTTATTTATACACATTAACATTA 90101  
QY 2732 TATTAACAATTAATTTTATTTTCTTCAATGCTTACTTAATTAATTAATCATTTTA 2791  
Db 90100 TGCAATTAACAATTTCTTTTACTTCAAAATGCTTGCACAAATCATAGACATTAATTTA 90041  
QY 2792 TTTTCTGAGGAAAGCATATCACTTTTATAGTATGAGTAAATTAATTAATTTTCA 2851  
Db 90040 ACTTTAGAG- -AAGTAACATTAATTTTAAATGATGAGTAAATTTTACTTA 89984  
QY 2852 CTTAAATTTATTTTAAAGTTTCAATTAAGATTAAGATTAAGTATTA- - 2908  
Db 89983 TTTTAATCAAACTT- -GGTTTCAATTAATGATGATGATCGATTCAGGTGACTC 89927  
QY 2909 - -TGTATTTGTAATAAGTTTAAATTTTTCGATGTCAATACAGCTTTATTTCA 2966  
Db 89926 TCTGTTATTTGTAACCAAGCTTTAAATTTTCAATTTTCAATATCTTTATTTT 89867  
QY 2967 TAGATTTATCTTTTAAAGATGATGATGATGATGATGATGATGATGATGATGAT 3026  
Db 89866 CGGATTTATTTCTTTTATGAGTATGAGTATGATGATGATGATGATGATGATGATGAT 89807  
QY 3027 TACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3086  
Db 89806 TACTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 89747  
QY 3087 AGCAAGAGCAATCAGATCCGACGACATTTGTCTCATCAAGTTGAATATAAAG 3146  
Db 89746 AGCAAGAGCAATCAGATCCGACGACATTTGTCTCATCAAGTTGAATATAAAG 89687  
QY 3147 CCACTTGAATACATTAATAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 3206  
Db 89686 CCACTTGAATACATTAATAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 89627  
QY 3207 GGAATTAAGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 3266  
Db 89626 GGAATTAAGTTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 89567  
QY 3267 GAAACAAGGAAAGATTTGATTTGATTTTAAACCATGCAAAATCTGCAATCTCTGTTTA 3326

Db 89566 GAAACAAGGAAAGATTTGATTTTAAATCATGACAGACTGCAAAATCTGTTTA 89507  
QY 3327 TATTTACCTTTTATGCTGATTTGCTGCGCCAGTGTGATCTGAATGAGAACAGCGACA 3386  
Db 89506 TATTTACCTTTTATGCTGATTTGCTGCGCCAGTGTGATCTGAATGAGAACAGCGACA 89447  
QY 3387 GAA 3389  
Db 89446 AAA 89444

Search completed: March 31, 2005, 12:46:14  
Job time : 9658 secs

**THIS PAGE BLANK (USPTO)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 07:28:21 ; Search time 1147 Seconds  
(without alignments)  
17496.010 Million cell updates/sec

Title: US-09-743-312d-1\_COPY\_7103\_10492

Perfect score: 3390  
Sequence: 1 tgcgtccgacgacatag.....atgagacagcgacgaag 3390

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

## SUMMARIES

| Result No. | Score  | *<br>Query Match | Length | DB | ID        | Description         |
|------------|--------|------------------|--------|----|-----------|---------------------|
| 1          | 3390   | 100.0            | 10492  | 3  | AAZ58843  | AAZ58843 Nucleotide |
| 2          | 1462.2 | 43.1             | 3438   | 4  | AAAC91773 | AAAC91773 Human myo |
| 3          | 525    | 15.5             | 2482   | 4  | AAFS6861  | AAFS6861 Murine my  |
| 4          | 508.6  | 15.0             | 5790   | 2  | AAAX24464 | AAAX24464 Bovine my |
| 5          | 494.8  | 14.6             | 1537   | 4  | AAFS6862  | AAFS6862 Porcine m  |
| 6          | 422.4  | 12.5             | 649    | 3  | AAZ50110  | AAZ50110 Human gro  |
| 7          | 332.8  | 9.8              | 1537   | 4  | AAFS6862  | AAFS6862 Porcine m  |
| 8          | 259.4  | 7.7              | 396    | 3  | AAZ50113  | AAZ50113 Mouse gro  |
| 9          | 190    | 5.6              | 2823   | 12 | ADH11572  | ADH11572 Human bon  |
| 10         | 174.4  | 5.1              | 200    | 4  | AAFS6863  | AAFS6863 Murine bo  |
| 11         | 141.8  | 4.2              | 156    | 3  | AAZ50115  | AAZ50115 Pig growc  |
| 12         | 136.2  | 4.0              | 336    | 2  | AAV89102  | AAV89102 EST clone  |
| 13         | 127.6  | 3.8              | 1195   | 2  | AAAX24415 | AAAX24415 Bovine my |
| 14         | 126.2  | 3.7              | 653    | 7  | ADDS31200 | ADDS31200 Human gen |
| 15         | 126.2  | 3.7              | 2742   | 2  | AAZ06449  | AAZ06449 Genomic D  |
| 16         | 126.2  | 3.7              | 2743   | 2  | AAV45813  | AAV45813 Human gro  |
| 17         | 126.2  | 3.7              | 2743   | 2  | AAZ09365  | AAZ09365 Human GDF  |
| 18         | 126.2  | 3.7              | 2743   | 4  | AAAF63550 | AAAF63550 Human GDF |
| 19         | 126.2  | 3.7              | 2743   | 6  | ABK15393  | ABK15393 cDNA enco  |
| 20         | 126.2  | 3.7              | 2743   | 6  | AAD29742  | AAD29742 Human pro  |

|    |       |     |        |    |           |                     |
|----|-------|-----|--------|----|-----------|---------------------|
| 21 | 126.2 | 3.7 | 2743   | 10 | ABQ76696  | ABQ76696 Human pro  |
| 22 | 126.2 | 3.7 | 2743   | 12 | ADM16470  | ADM16470 Human pro  |
| 23 | 126.2 | 3.7 | 2743   | 12 | ADM16493  | ADM16493 Human pro  |
| 24 | 126   | 3.7 | 1239   | 2  | AAAX24416 | AAAX24416 Bovine my |
| 25 | 124.6 | 3.7 | 2743   | 2  | AAQ76372  | AAQ76372 Human gro  |
| 26 | 118.4 | 3.5 | 799    | 3  | AAZ50114  | AAZ50114 Chicken g  |
| 27 | 115.2 | 3.4 | 564    | 2  | AAV89872  | AAV89872 EST clone  |
| 28 | 111.8 | 3.3 | 749    | 4  | AAH04272  | AAH04272 Human CDN  |
| 29 | 111.8 | 3.3 | 2277   | 4  | AAH15506  | AAH15506 Human CDN  |
| 30 | 104.6 | 3.1 | 2100   | 3  | AAAG0289  | AAAG0289 Mouse wil  |
| 31 | 104.6 | 3.1 | 2171   | 6  | AAD29743  | AAD29743 Murine pr  |
| 32 | 104.6 | 3.1 | 2675   | 2  | AAZ06448  | AAZ06448 Genomic D  |
| 33 | 104.6 | 3.1 | 2676   | 2  | AAQ76371  | AAQ76371 Mouse gro  |
| 34 | 104.6 | 3.1 | 2676   | 2  | AAV42113  | AAV42113 Murine gr  |
| 35 | 104.6 | 3.1 | 2676   | 2  | AAZ09364  | AAZ09364 Murine GD  |
| 36 | 104.6 | 3.1 | 2676   | 4  | AAAF63549 | AAAF63549 Murine GD |
| 37 | 104.6 | 3.1 | 2676   | 6  | ABK15394  | ABK15394 cDNA enco  |
| 38 | 104.6 | 3.1 | 2676   | 8  | ABK15456  | ABK15456 cDNA enco  |
| 39 | 104.6 | 3.1 | 2676   | 10 | ABQ76697  | ABQ76697 Murine pr  |
| 40 | 104.4 | 3.1 | 330973 | 11 | ACN44846  | ACN44846 Human gen  |
| 41 | 103   | 3.0 | 2676   | 2  | AAAX24417 | AAAX24417 Mouse myo |
| 42 | 102.8 | 3.0 | 355    | 4  | AAI93466  | AAI93466 Human can  |
| 43 | 100.4 | 3.0 | 25000  | 12 | ADJ34524  | ADJ34524 Human GUC  |
| 44 | 96.2  | 2.8 | 348101 | 12 | ADQ97146  | ADQ97146 Human can  |
| 45 | 95.2  | 2.8 | 22475  | 12 | ADQ97998  | ADQ97998 Human can  |

## ALIGNMENTS

|          |                                                                    |
|----------|--------------------------------------------------------------------|
| RESULT 1 |                                                                    |
| AAZ58843 |                                                                    |
| ID       | AAZ58843 standard; DNA; 10492 BP.                                  |
| XX       |                                                                    |
| XX       | AAZ58843;                                                          |
| XX       |                                                                    |
| DT       | 25-APR-2000 (first entry)                                          |
| XX       |                                                                    |
| DE       | Nucleotide sequence of bovine myostatin promoter-enhancer region.  |
| XX       |                                                                    |
| KM       | Myostatin; promoter; muscle cell disorder; genetic marker; bovine; |
| KW       | myogenic regulatory factor; oncogene; muscle growth;               |
| XX       | muscular dystrophy gene; ss.                                       |
| XX       |                                                                    |
| OS       | Bos sp.                                                            |
| XX       |                                                                    |
| FH       | Key                                                                |
| FT       | enhancer                                                           |
| FT       | Location/Qualifiers                                                |
| FT       | 9094. .9099                                                        |
| FT       | /*tag= a                                                           |
| FT       | /note= "E-box 4"                                                   |
| FT       | 9236. .9241                                                        |
| FT       | /*tag= b                                                           |
| FT       | /note= "E-box 3"                                                   |
| FT       | 9860. .9865                                                        |
| FT       | /*tag= c                                                           |
| FT       | /note= "E-box 2"                                                   |
| FT       | 9879. .9885                                                        |
| FT       | /*tag= d                                                           |
| FT       | /note= "TATA-box 3"                                                |
| FT       | 10095. .10100                                                      |
| FT       | /*tag= e                                                           |
| FT       | /note= "E-box 1"                                                   |
| FT       | 10197. .10201                                                      |
| FT       | /*tag= f                                                           |
| FT       | /note= "CAAT-box"                                                  |
| FT       | 10240. .10246                                                      |
| FT       | /*tag= g                                                           |
| FT       | /note= "TATA-box 2"                                                |
| FT       | 10264. .10270                                                      |
| FT       | /*tag= h                                                           |
| FT       | /note= "TATA-box 1"                                                |
| FT       | 10403. .10492                                                      |
| FT       | /*tag= i                                                           |
| CDS      |                                                                    |

|    |                                                                        |
|----|------------------------------------------------------------------------|
| FT | /note= "partial coding fragment"                                       |
| XX |                                                                        |
| PN | MOZ00001810-A1.                                                        |
| XX |                                                                        |
| PD | 13-JAN-2000.                                                           |
| XX |                                                                        |
| PF | 07-JUL-1999; 99MO-NZ000107.                                            |
| XX |                                                                        |
| PR | 07-JUL-1998; 98NZ-00330902.                                            |
| XX |                                                                        |
| PA | (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.                       |
| XX |                                                                        |
| PI | Baas J.J., Jeonplong F., Kambadur R., Sharma M,                        |
| XX |                                                                        |
| DR | WPI, 2000-182112/16.                                                   |
| PT | Novel promoter sequences of the myostatin gene used to diagnose muscle |
| PI | cell disorders.                                                        |

CC The invention relates to a bovine myostatin promoter sequence. The  
CC myostatin promoter polynucleotide sequences can be used in diagnostic  
CC tests for muscle cell disorders, and as a genetic marker for the  
CC selection, in particular, of cattle and sheep breeds that express low  
CC levels of myostatin, and so have increased muscle mass. The promoter can  
CC also be used for the transcriptional control of a heterologous gene of  
CC interest, e.g. myogenic regulatory factors, myostatin and myostatin  
CC receptor, oncogenes, genes that regulate muscle differentiation and  
CC growth, the muscular dystrophy gene, and any other genes expressed in  
CC muscle. The present sequence represents the nucleotide sequence of bovine  
CC myostatin promoter-enhancer region  
XX  
SQ Sequence 10492 BP, 3262 A, 2160 C, 2002 G, 3068 T, 0 U, 0 Other;

|                       |                |              |          |              |
|-----------------------|----------------|--------------|----------|--------------|
| Query Match           | 100.0%         | Score 3390   | DB 3     | Length 10492 |
| Best Local Similarity | 100.0%         | Pred. No. 0  |          |              |
| Matches 3390          | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0       |

|    |      |                                                                 |      |
|----|------|-----------------------------------------------------------------|------|
| OY | 1    | TGCTCTCCGAAGCCATGAGGAAAGTGTGCAATCCCGGCACTGGAAGAAACACGTTCC       | 60   |
| Db | 7103 | TGCTCTCCGAAGCCATGAGGAAAGTGTGCAATCCCGGCACTGGAAGAAACACGTTCC       | 7162 |
| OY | 61   | TTGAAATTTCTTGAGTACCTCTTAATTCATTCATGCTGACCTCCGAGATTGATAGAG       | 120  |
| Db | 7163 | TTGAAATTTCTTGAGTACCTCTTAATTCATTCATGCTGACCTCCGAGATTGATAGAG       | 7222 |
| OY | 121  | CTGACTCTCATATTCAACAGTGGTATGTTCTACCCAACTCACTGCCAACATGAATAGTG     | 180  |
| Db | 7223 | CTGACTCTCATATTCAACAGTGGTATGTTCTACCCAACTCACTGCCAACATGAATAGTG     | 7282 |
| OY | 181  | ATTCTGAACCACTCCCTAGGGGAATTCAAGGTATGATCCGTCAGCTCTGGTCA           | 240  |
| Db | 7283 | ATTCTGAACCACTCCCTAGGGGAATTCAAGGTATGATCCGTCAGCTCTGGTCA           | 7342 |
| OY | 241  | CGTTTTTGTAAACAATCAATTAATTAACCTGTGTTGTGCATTTCTGTTTAAATAT         | 300  |
| Db | 7343 | CGTTTTTGTAAACAATCAATTAATTAACCTGTGTTGTGCATTTCTGTTTAAATAT         | 7402 |
| OY | 301  | CTTTATTTAATACGTAAGTCTTAATTTCTCAACATTTGGTTCAACACAAAGGCTTAT       | 360  |
| Db | 7403 | CTTTATTTAATACGTAAGTCTTAATTTCTCAACATTTGGTTCAACACAAAGGCTTAT       | 7462 |
| OY | 361  | AACGTGAAGCCCTGAATGAGGTTACATTAACAACAATGTTTTTGTATAGGAAAAATTT      | 420  |
| Db | 7463 | AACGTGAAGCCCTGAATGAGGTTACATTAACAACAATGTTTTTGTATAGGAAAAATTT      | 7522 |
| OY | 421  | TTCTCTTCAAGCTCTGCACAAGCCTTCTGCTTAATTAATTTGACCAAAATATACATTAACATG | 480  |
| Db | 7523 | TTCTCTTCAAGCTCTGCACAAGCCTTCTGCTTAATTAATTTGACCAAAATATACATTAACATG | 7582 |
| OY | 481  | AAACGTACTATTTTAACGTATTTTAACGTACAGTTCAGTGGCATTAAGTACCTTAC        | 540  |



PR 10-JUN-1999; 9905-00329685.

XX (ABBO ) ABBOTT LAB.

PI Wu-Mong JR, Wang J,

XX WPI; 2001-071272/08.

XX Promoter which regulates expression of myostatin gene, whose inhibitors  
PT are useful for preventing conditions involving muscle wasting such as  
PT cancer, multiple sclerosis, aging and acquired immune deficiency  
PT syndrome.

XX Claim 1; Fig 2; 31pp; English.

CC The invention relates to the human myostatin promoter. Myostatin (also  
CC known as growth/differentiation factor 8 and GDF8) is a member of the TGF  
CC-beta superfamily and is a negative regulator of skeletal muscle growth  
CC and development. The invention also encompasses a reporter plasmid  
CC comprising a reporter gene operably linked to the human myostatin  
CC promoter, and host cells comprising the reporter plasmid. The invention  
CC further relates to an antibody against human myostatin. The invention  
CC screening for compounds which inhibit myostatin promoter activation,  
CC which inhibit myostatin expression, or which interfere with the binding  
CC of myostatin to a myostatin receptor. Compounds which inhibit myostatin  
CC expression or function are useful for preventing disorders which involve  
CC muscle wasting, such as AIDS, cancer, multiple sclerosis and aging. Anti-  
CC myostatin antibodies may also be used in veterinary medicine to prevent  
CC muscle wasting in ageing or diseased animals, and in agricultural  
CC applications to increase meat production in livestock. The present  
CC sequence represents the human myostatin promoter

XX SQ Sequence 3438 BP; 1151 A; 628 C; 568 G; 1091 T; 0 U; 0 Other;

Query Match 43.1%; Score 1462.2; DB 4; Length 3438;

Best Local Similarity 72.7%; Pred. No. 5.2e-277;

Matches 2475; Conservative 0; Mismatches 743; Indels 187; Gaps 38;

QY 1 TGCTGCTCCGAGCCATAGAGAGGTTGCAATCCCGGCACTGAGAGAGAAACACGCTC 60  
DB 119 TTCTATTCTGGGGCTCAGAGAGGTTGCAATCACTGCGCATGAGAGAAATAAACTTA 178  
QY 61 TTGAAATTTCTTGAGTACCTTCTTAACTTCAATGCTGACCTCCGA-----GATTGG 114  
DB 179 CTTAAATTTCTTCACTTCTTCAACCATTCATCTGTTCTCTAAGAGAGTTGATTAG 238  
QY 115 ATAGAGTGACTCTCATTTTACAGGTGTTATGTTTACCAATCACTGCGCAACA-TGA 173  
DB 239 ATATAGTCAATTTCTCCCTATTCATAGTATGTTCTATTAAGTCACTGCGCAACTGA 298  
QY 174 ATAGAGTATCTGAAACCACTGCCCCCTAGGGGAACTCAAGAGTTAGATCCCGTCACT 233  
DB 299 GTTAGCAAAATATGAATATATGTTCCAGGGGAAAAACAGGTTAGTTAGCCCTG--- 355  
QY 234 CTGCTACGTTTTTGTTAACCAATGATTAATACCTTTGTTGTGCACTTTCTGTTTT 293  
DB 356 GTATATACATTTATCATCAACCAATATATTAACCTGTTTATATGATGTTTTTGTTTA 415  
QY 294 AAAATATCTTATTTATAGTACTGCTAAATCTTCAACATTTGTTGTCACACCAAAAG 353  
DB 416 CAATAA-CATTATTTATATATATTTGTTCACTTCACTGAACCTCAAGCCA-----G 470  
QY 354 CCTTATTAAGTGAAGCCCTGAATGAAGCTTATACATACACATGTTTCTATAGAGA 413  
DB 471 CAGCAGTATTAACCTGAGCTGAAATGATGCTTATCTACACA---TGCAATTTTTCAGAG 527  
QY 414 AAAATTTTCTTCACTGCTGCGACAGCCTTCTTCTTAATTTGTCAGCAAAATATACA 473  
DB 528 AACTTTTTTCTTAGGCAATATCAAGCCTT-----TTAAATATGTTGTAATATATACA 582  
QY 474 TAACATGAAGCTGATTTATTTAAGTATTTAAGTCACTGATGCTGAGTGAAGTAACTA 533  
DB 583 ACATTTAGCA-----TCTTAAACATTTTATGTTGTTACAGTTCCGTTGCAATTAAGA 633

QY 534 CACTTACCTTGTCTGGAACTATGATCAATTCATCTCTAGAACCTTTTGTCTCTCG 593  
DB 634 CATTACACTGTTGTGTAACCATCACACCATTCATCTGAAATTTTTCATCTTCCCA 693  
QY 594 AATTGAAATCTTGATCTATTGACAGTAGTACTTCCCATCAACCCGACCTTCTCTC 653  
DB 694 GACTG--AACTGTATCTATCAACAGTAACTAACCTTCA-----GTGCTTACCC 743  
QY 654 CAGCCCCCGGCAACCATCTTCTTTCATGACAGTCACTGCTGCTAGGAACA--- 710  
DB 744 CAGTCCCTGGCAACCACTGCTAATCTTCCATTCAGCCTTTCTGTGATTTAGAACATAG 803  
QY 711 -----CAGCCTTCAACACTACGCTTGGGGGCACTGT-----AGCAACAGATC 756  
DB 804 GAACACAGCAGCAGTCACTGACCTATGCTTGGGGGCAATTTTAAAGCAAAATCAAT 863  
QY 757 ACTGCTTACCGCCACCAATGCAACAAATATTAAGACATGTGGCATATGATTC 816  
DB 864 AAGAGGCAATTAATAAAGAACCAAAATATGTGAAACATGCGACTAAATAGACGGG 923  
QY 817 AAAAGGCTGCTGCT--AGTATGAGGGCTGAAC--AAGCAGAAATGACTAGT 871  
DB 924 AAAAGGAAATTTGTTTATATGATGAGCTGAACAAAGGCGAACCCTGCTTGT 983  
QY 872 TGACTCAGCTGGGATCTGTGTGTGG--AGCCTCAATTTTCCATTTGCTGTGAT 929  
DB 984 TGACCTCATCTGGGAACCTGTGCTGATAGAGACTCAAAATTTTTCGCGCTGTGAAT 1043  
QY 930 AGCACAATGCTTATTAAGCACTGTAGAGATTGATTAAGATTAAATATCTCAG 989  
DB 1044 GCCAGCAATGACTGAAAAA---TGCTAGAAATATGAGTTTCATAGATTAATTTTACG 1099  
QY 990 CAAGACATAAATGTGCAAGCAGGATCCATGATTAACAGCACTGACCAT--GTGGAA 1047  
DB 1100 AAGTAGCAAAATTTGTGAATACGAATATCATGATTAATTAAGATTGCTTACGGAAA 1159  
QY 1048 TGATTAATCTTGTCTTCTTATTTCAAGCAGTAAAGAAAGGCG-----T 1093  
DB 1160 TGACAACTTTGTTCACTTTTCCAGGTGATTAAGATTAAGAGCTGGAACATGCTGTG 1219  
QY 1094 CAGAGGCTGCTTACACCATTTTACTAGAGACTGACCTATGCTAGTGG----- 1144  
DB 1220 AACCTGCTGCTTAAAGAAATTTTACTTGTGCTCAAGGCTTAAGAAAGTGGCTTTGTGAC 1279  
QY 1145 ---TAGTGGCAATTAACAACTGAAGCAAGTTCTAGTCAATGTGAGAGATTAACCA 1201  
DB 1280 TGATTAATGCACTATGACCTTAAGCAAGTTCTAGTTCATGTGAGCATTAATTTAAGCA 1339  
QY 1202 TAATCTCAACCCCTCTGCAAGAAAGAGACTAAGTACTCAAGTACAGTACAGTCA 1261  
DB 1340 TAATCTCAACCCCTCTGCAATTAACAAAGAGCAAGCACTCAATGCGCAAGTTCAATTA 1399  
QY 1262 CTACTATATGAGAGCACTGTACTCAACATTTTACATGATTTATGATTAATGATCCCC 1321  
DB 1400 CTTACTATATGAGAGGTCATATTTCAAGCAATTTTACATGATTTAAATTAATCCCCC 1459  
QY 1322 CACACCTATAGAGAGCTGAAGTTAGAG-----AGTATCTCACTTATTAACACA 1376  
DB 1460 CAAAACCTATAGAGAGCTGAAGTTTGAAGAGTTAAGTATCTTCACTTATTCACATA 1519  
QY 1377 GT-----GGCAACCTGAGATCTGAACCTCAGGTATATCACTCCAGGACCTGAGATC 1428  
DB 1520 GTTAAAGAGGCAAGGTGAGATTGAACCTCAGGTCTATCTGCTCAAGGCTGAGTTC 1579  
QY 1429 CCAATGCTACACAAATTTCTATCAAGTTAAAGGAAAAAGATTTGATTTGCTCGAAG 1488  
DB 1580 TCAATTTCACTGCTATACAAATTTCTAAGCATTTAAAGAAAAAGTTTGAATTTAGTGAAC 1639  
QY 1489 TGATATGAGGCAATATGTAACA---ATTATTAACATTAAGAAATTTATGTTGAAGAAATA 1545  
DB 1640 TGATATGATGCAATGTGTTCAATGATCATTAACATTTGAAGATTTTACATTTGAAGAAATG 1699



XX (PRIZ ) PRIZER PROD INC.  
 XX Findly RC;  
 XX WPI; 2001-170964/18.  
 DR  
 XX Novel myostatin gene promoter for regulating expression of heterologous  
 PT genes in cells or animals, for identifying compounds that inhibit its  
 PT activity or expression, which are useful for treating muscle disorders.  
 XX  
 PS Claim 1; Fig 1; 24p; English.  
 XX  
 CC The present sequence is an isolated myostatin gene promoter. Regulating  
 CC the transcription activities or expression of the promoter is useful for  
 CC treating muscle associated disorders such as cancer, muscular dystrophy,  
 CC spinal cord injury, neurodegenerative disorders, traumatic injury,  
 CC congestive obstructive pulmonary disease (COPD), amyotrophic lateral  
 CC sclerosis, acquired immunodeficiency syndrome (AIDS), cachexia or ageing.  
 CC The promoter is useful for modulating the expression of the myosin gene  
 CC for producing animal food products having increased muscle and protein  
 CC content and reduced fat and cholesterol content, for regulating  
 CC expression of a heterologous gene in cells or animals, for engineer host  
 CC cells, to screen for compounds that inactivate or inhibit its  
 CC transcription and expression, for inhibiting its expression in cells for  
 CC the promotion of muscle growth, for diagnostic evaluation, genetic  
 CC testing and prognosis of a disease or disorder associated with myostatin  
 CC expression  
 CC  
 SQ Sequence 2482 BP; 784 A; 519 C; 474 G; 705 T; 0 U; 0 Other;  
 Query Match 15.5%; Score 525; DB 4; Length 2482;  
 Best Local Similarity 61.5%; Pred. No. 3.7e-93;  
 Matches 1256; Conservative 0; Mismatches 665; Indels 122; Gaps 21;

QY 1188 GATGAATTTACCAATCTCAACCCCTCGCATGAAACAGACATCAAGTCAAGTA 1247  
 DB 521 GAACACCTTGAGATTAATTTGAAAGTAAAGAGCTTGAAACAAAGAGAGCCCTTCTGCT 580  
 QY 1248 CCACTTACAGTCACTTACTATATG-----ACAGGCACTGTACTCAACATTTTCAAT 1289  
 DB 581 TCAAGTATTAATTAACCTATGAAAGGAGCTACATTTAGTACTTATATGCTAAATTTATAT 640  
 QY 1300 GTATTAATTTGAATTCAGTCCCAACCACTATGAGAGAGCTGAAGTTAGAGAAATTC 1359  
 DB 641 GCCCTCAACCCCTTATGTTAGAAACCTAAGATTAAGAGAGCTAAGTACTGCGCTT 700  
 QY 1360 TCATTCAATTTATACAGAGTGGCAACAGAGATCTGAAGTCAAGTCAATCCACAGGA 1419  
 DB 701 TGTATGATGATTTAAGAGAGGCAAAATGAGATTTGAAGTCAAGTTATTTGACTCTTCAG 760  
 QY 1420 CTTGAGATTCCTAATTTGCTACAAATTTCAATCAAGTTAAAGGAAAAAGATTGATTT 1479  
 DB 761 TCTAGCTCAAAATGGGAGTACAGTCTAABAAAAAATCAAGATCA-----ATT 816  
 QY 1480 GCTCAGAGTGTATAGGGGCAATATGTTAC--AAATTAACATTACAAAGATTTATATGT 1536  
 DB 817 CCTCTGAGTATATAGAGCATGTGTATATGATTAATTTGACATGAAAGAAATTTATATGC 876  
 QY 1537 TGAATAATTAATTTATCAAAATTAATTAATTTAAGCTTGAATTAATCTGCTCCGCA 1586  
 DB 877 AGAAAAATGAAATTTTCCAGAAATTTGACTTTAAGGCTGCTCAATATATTTGCTTGTGA 936  
 QY 1597 ACAAGATATCTGAAATCTTTGAGGCACTGTTTGTGCTGTTTCTTATCTTT 1656  
 DB 937 --TAAAGAGGCGCAGATCACTCAAGGCTGCTGTTGCTGCTGTTTCTTATCTTT 994  
 QY 1657 AATGATGGGCAATCTAATGATATGATAGGCA-----TTTTTCTCAAGAGATGATG 1711  
 DB 995 AATGATGGGCAATCTAATGATATGATAGGCA-----TTTTTCTCAAGAGATATGATG 1054  
 QY 1712 ATACCTTTAAGATTTGATGAAATGATTAATTTTCAAGGCTACGATGATGATTTTA 1771  
 DB 1712 ATACCTTTAAGATTTGATGAAATGATTAATTTTCAAGGCTACGATGATGATTTTA 1771

DB 1055 ATGCCCTTTAAAAATTTGATGAAATGATTAATTTTCAAGCTACGAGCTGATTTTA 1114  
 QY 1772 GTGCACTGAGGCAAGTAATTT--AGTGTACATGTGCGAAAGTACCTTAATAATAA 1828  
 DB 1115 GTTCACTGAGGCAATTAATTTGGTGTATATCTGATCAGAAATGTGTGATGACCTTAATAATA 1174  
 QY 1829 ATATTGATATGAACCACTGCACTCTTTGGGG-----AAAAAGTAATGATTAAC 1880  
 DB 1175 ATATTGATATCAAGCCACATAGTCTTCTGGGGGTGTGTATGAGGGGATATGATTAATA 1234  
 QY 1881 TCTCTTGAAGTCTTGTAGCTTCCCAAAAGATGAGAAAAATTAATCTCTGGGGCTG 1940  
 DB 1235 ATTTAAAGACTCTTCAAGCTTCCAAACAGAGAGAA-----CTTGTGGGCTG 1285  
 QY 1941 GAACACCTTCTGTTCTTCTGCTGCTAATTTGTTAGTTTATATAGTCAATTTGAT 2000  
 DB 1286 GAACGCTCTGTGCTCT--GCTGCTGTTTGTTCAGCTCTTTAAGAGTTACCCCAT 1343  
 QY 2001 AGACCTTGTGCTCCCAAGCTAAGTTGAGAGTTGATCTTACAGAGGCACTTCAAT 2060  
 DB 1344 CGATCTTGTGCTCTTAAGCCAAAGGAGTGAAGTTGATCTTGCAGAGGCACTTAAT 1403  
 QY 2061 TTAAAGAAACAAAGCCCAATCTCTGCTCCAGACCTTAACCCCAATCTCTGCAAGTG 2120  
 DB 1404 TCAGAGAAACAAAGAACCAATCTCTGCT--CCTAAGCTCTAAGCCCAAGTCTCTGCAAGTG 1462  
 QY 2121 TCTGCTCTGCTGCTCAATGAGAAACCTGCAAGAGAAATCAAGAGGCTGCAAGTACTA 2180  
 DB 1463 TCTGCTCTTGTGTAAATGAGAGCTGCGCAAGAGGAGTGTGATCTTGCAGAGTAT---- 1518  
 QY 2181 GGAAGTAAAGAAATGAGCTAGACACTAGAGAGAGAGAAATGGGCAACCTTCATGA 2240  
 DB 1519 -----GGAAAGCAACAAAGAGACACCCCTTACA 1547  
 QY 2241 TGTGTTCTTCTCCCTTCTGTGTGTCACATGCTCCGATTAATTTACAGAGGTATATA 2300  
 DB 1548 ---TGCAGCTGCTTGTGTGTGTCTAC--GGAGCTGACATCTTCAAGAGAACACAGA 1603  
 QY 2301 ACTACATTTTCTTTTCAACACTGAGAGGCTGAGAAACCTTGTGTA-----CCC 2351  
 DB 1604 ---TTGACATTTTCTGACAGCCCTGAGAGTGTAGTGAATGAATTAATGCTCCAGCGC 1660  
 QY 2352 ATCATTAATTTCACTATCTTCTAAGTATCTATGTTATTTATTAAGTCAATATGCTGACA 2411  
 DB 1661 TACTTACAAATTCATATATCTAATCTGAGGCTAAGTACAGAGCTGCTGCTGCTGACA 1720  
 QY 2412 ATATCCTTTGTATTAACAAATGAAGAAACACATCTCTGAGAAATTAATCTGAGAC 2471  
 DB 1721 GGAATCTGTGTGCAATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1780  
 QY 2472 TTTAGATGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2531  
 DB 1781 ATCTCTGTATTAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1840  
 QY 2532 ATTAAGATTAAT--TTAAAGTATTTCAATGAGCAATTAATTAATTAATTAATTAATTAAT 2586  
 DB 1841 GTCAAGGCAATTAAGTATCAAAAGTAAACCCATGTATACAGAAACGCTCCAGAGATGCT 1900  
 QY 2587 TTTCAATATGTTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2646  
 DB 1901 TTGTAAATATGCTGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1960  
 QY 2647 CTTTAACTATATACAGTCTTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2706  
 DB 1961 TTTTAAAGAGGTACAAACCTGACCTTTCTTAATTAATTAATTAATTAATTAATTAATTAAT 2020  
 QY 2707 TTAATCAAGACTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2766  
 DB 2021 TTCT-----CTAATTAACGAGCACTTAAGCATTAATTTTCTCTCAAAATTAATTAAT 2068  
 QY 2767 ACTTAATATGATTAATTAATTAATTTATTTTGTGAGGAGAAAGATTAATCACTTTTAAGTA 2826  
 DB 2069 GTTTTGTAAACAAAGCACTCAAGTCTCAAGAGATTAATTAATTAATTAATTAATTAATTAAT 2127







| OS | Homo sapiens.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                                                      |
|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| XX | Key                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Location/Qualifiers                                                  |
| XX | mutation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | replace(284..289, agatct)                                            |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /*tag= b                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /note= "Mutation resulted in 25% decreased luciferase activity"      |
| FT | misc_feature                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 331..486                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /*tag= a                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /note= "Portion of promoter element which is claimed as SEQ ID NO:6" |
| FT | mutation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 393..398                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /*tag= c                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /note= "Mutation resulted in increased luciferase activity"          |
| FT | mutation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 413..418                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /*tag= d                                                             |
| FT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /note= "Mutation resulted in 40% decreased luciferase activity"      |
| XX | WO200004051-A2.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                      |
| XX | 27-JAN-2000.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                      |
| XX | 15-JUL-1999;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 99WO-US016026.                                                       |
| XX | 15-JUL-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 98US-0092865P.                                                       |
| XX | 08-MAR-1999;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 99US-0123270P.                                                       |
| XX | (META-) METAMORPHIX INC.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                      |
| XX | Liáng L;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                      |
| XX | WPI; 2000-182405/16.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                      |
| DR | Novel promoter sequence for tissue specific gene expression in gene therapy, for treating muscle associated disorders, e.g. muscular dystrophy.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                      |
| PT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                      |
| PT |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                      |
| PS | Claim 4; Fig 2; 40pp; English.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                                                      |
| XX | The patent discloses the use of growth differentiation factor (GDF) gene promoters for tissue specific gene expression in gene therapy. These elements are located upstream of the 5' end of a GDF gene. GDF promoters ensure proper binding and activation of RNA polymerase and influence transcription levels. They are used for muscle specific expression of a gene by transfecting it into a muscle cell and thus treatment of muscle associated disorders e.g. cancer, muscular dystrophy, spinal cord and traumatic injury, congestive obstructive pulmonary disease, AIDS, cachexia, and obesity or its related disorders (e.g. diabetes) and disorders related to abnormal proliferation of adipocytes by gene therapy. The present sequence is human GDF-8 promoter element used in the construction of luciferase reporter construct pGL-3-basic for modifying luciferase activity. This construct is used in screening for regulatory compounds of GDF expression |                                                                      |
| XX | Sequence 649 BP; 240 A; 89 C; 95 G; 225 T; 0 U; 0 Other;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |                                                                      |
| XX | Query Match                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 12.5%; Score 422.4; DB 3; Length 649;                                |
| XX | Beet local Similarity                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 82.0%; Fred. No. 3.7e-73;                                            |
| XX | Matches 536; Conservative                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 0; Mismatches 111; Indels 7; Gaps 4;                                 |
| OY | 2652 ACTAGTATCAGAGCTTTTCATTATTAAGC-TTCCGATTAATATCGTATTTTCAATAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 2710                                                                 |
| DB | 1 ACTAGTATCATAATCTTTAACTTTTAACTCAGGCTTCTCTAATTTTATTTTCTTAATTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 60                                                                   |
| OY | 2711 ACAAGACTAAATAATTAATTAATTAACAATAATTAATTTT-TACTTCAATGCTTACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 2769                                                                 |
| DB | 61 TTGGCACTAAATAATTAATTAATTAATTAACAATAATTAATTTTCTACTTCAATACTTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 120                                                                  |
| OY | 2770 TAAATAGTAAATTAATCATTTTATTTTTCGAGGAGAAAAGCATATCAACTTTTAAAGTATGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 2828                                                                 |
| DB | 121 TAAACAAATATAAATCATTTTAAAGTTTTCGAGGAGTAATATTTTC-ATATTTTAAATATGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 179                                                                  |

|          |                                                                            |                                                               |      |
|----------|----------------------------------------------------------------------------|---------------------------------------------------------------|------|
| QY       | 2830                                                                       | AGTGTAAATTAAGATTATTAATCACTTAATTAATATTTTAAAGTTTCACATATAAGATG   | 2889 |
| Db       | 180                                                                        | AGTATAATTTAAATTGACTTATTTAAATTTCATTAAGAGCTGTGTGAGATTGTAGA      | 239  |
| QY       | 2890                                                                       | AATAAGATCTTAGTGATATGTATTTGTATAATAAGTTTAAATTTTTCGATGTCAAT      | 2949 |
| Db       | 240                                                                        | TTTAAAG----TACAGTTTATATTAATGTGCAACATAGACTTTTGTTTTCAAAATGTACAA | 295  |
| QY       | 2950                                                                       | ACAGCCTTATTAATTCATAGATTATTCCTTTTAAGAATAGTCAAAATGATCGCTCAC     | 3009 |
| Db       | 296                                                                        | ATATCTTTTATTAATTTGTAGATTATTTCTTTTATGAAGTAGTCMAATGAAATCAGCTCAC | 355  |
| QY       | 3010                                                                       | CCTTGACTGTAAACAAATATCTGTTTGGAGACTTGTGACAGACAGAGGTTTAACTCTGCAC | 3069 |
| Db       | 356                                                                        | CCTTGACTGTAAACAAATATCTGTTTGGAGACTTGTGACAGACAGAGGTTTAACTCTGCAC | 415  |
| QY       | 3070                                                                       | AGCGAGATTCATTTGTGAGCAAGAGCCCATCAAGATCCGACGACACTTGTCTCATCAA    | 3129 |
| Db       | 416                                                                        | AGCGAGATTCATTTGTGAGCAAGAGCCCATCAAGATCCGACGACACTTGTCTCATCTA    | 475  |
| QY       | 3130                                                                       | AGTTGGAATATTAATAAAGCCACTTGGATATACGTAATAAAGATTACCTGTGTGCAAGTT  | 3189 |
| Db       | 476                                                                        | AGTTGGAATATTAATAAAGCCACTTGGATATACGTAATAAAGATTACCTGTGTGCAAGTT  | 535  |
| QY       | 3190                                                                       | GTCCTCTGAGACTGGGCGGCACTTAACGTTTGGCGTTGCGTACTCAAAAGCAAAAGAAA   | 3249 |
| Db       | 536                                                                        | GTCCTCTGAGACTGGGCGGCACTTGAATACGTAATAAAGATTACCTGTGTGCAAGTT     | 595  |
| QY       | 3250                                                                       | GTAAGAAGGAAGTAAGAACAAGGGAATAATTTGATATTTTAAACCATG              | 3303 |
| Db       | 596                                                                        | GTAAGAAGGAAGTAAGAACAAGGGAATAATTTGATATTTTAAATCATG              | 649  |
| RESULT 7 |                                                                            |                                                               |      |
| ID       | AAFS58662/c                                                                |                                                               |      |
| XX       | AAFS58662 standard; DNA; 1537 BP.                                          |                                                               |      |
| AC       | AAFS58662;                                                                 |                                                               |      |
| DT       | 27-APR-2001 (first entry)                                                  |                                                               |      |
| DE       | Porcine myostatin gene promoter.                                           |                                                               |      |
| KW       | Porcine; pig; myostatin; promoter; cytosstatic; anti-HIV; neuroprotective; |                                                               |      |
| KW       | immunomodulator; cancer; muscular dystrophy; spinal cord injury;           |                                                               |      |
| KW       | neurodegenerative disorder; congestive obstructive pulmonary disease;      |                                                               |      |
| KW       | COPD; amyotrophic lateral sclerosis; acquired immunodeficiency syndrome;   |                                                               |      |
| XX       | AIDS; cachexia; aging; ds.                                                 |                                                               |      |
| OS       | Sus scrofa.                                                                |                                                               |      |
| PN       | EP1072680-AI.                                                              |                                                               |      |
| PD       | 31-JAN-2001.                                                               |                                                               |      |
| XX       | 27-JUL-2000; 2000EP-00306396.                                              |                                                               |      |
| XX       | 30-JUL-1999; 99US-0146540P.                                                |                                                               |      |
| PA       | (PE12 ) PFIZER PROD INC.                                                   |                                                               |      |
| PI       | Findly RC;                                                                 |                                                               |      |
| DR       | WPI; 2001-170964/18.                                                       |                                                               |      |
| PT       | Novel myostatin gene promoter for regulating expression of heterologous    |                                                               |      |
| PT       | genes in cells or animals, for identifying compounds that inhibit its      |                                                               |      |
| PT       | activity or expression, which are useful for treating muscle disorders.    |                                                               |      |
| XX       | Disclosure; Page 12-13; 24pp; English.                                     |                                                               |      |
| CC       | The present sequence was used for comparison studies with a myostatin      |                                                               |      |

| Query Match           | 9.8%                                                         | Score 332.8                                                  | DB 4           | Length 1537 |
|-----------------------|--------------------------------------------------------------|--------------------------------------------------------------|----------------|-------------|
| Best Local Similarity | 63.9%                                                        | Pred. No. 1.7e-55                                            |                |             |
| Matches 555           | Conservative                                                 | 0                                                            | Mismatches 302 | Indels 11   |
|                       |                                                              |                                                              | Gaps 3         |             |
| 2485                  | GTAACTTAATCTAGTCAATGAAACCTAAATACAAATTTTCATATGATGATTAAGATATTA | 2544                                                         |                |             |
| Db                    | 1223                                                         | GAACTTTAAATTCGTAATTTAAATGAATATCTTTTACACTTCACTTAAAAAGTTG      | 1164           |             |
| Qy                    | 2545                                                         | TTTAAAGTAATTCATGACATTTAATATTAAGTGAATTTTCATTATGTGTAGA         | 2604           |             |
| Db                    | 1163                                                         | AAATGCTCTTTTCCCAAAAAATTAATGATTTTACATTTATTAAGCAAAACATTTGGG    | 1104           |             |
| Qy                    | 2605                                                         | ATTATTCAGGAAACAAGTTCTCAATTTATAGCAGAAAATCTTTTCTGTATCACAG      | 2664           |             |
| Db                    | 1103                                                         | AAAAAAGAAATTTTATTTGCTGTTTAAATATTTTATGTCTGTGTAATCAGAGAAATAC   | 1044           |             |
| Qy                    | 2665                                                         | TCCTTTCAATTTAAGCTTCTCGTAATAAATCTGTATTTTCTAATTTATACAGACTAAAT  | 2724           |             |
| Db                    | 1043                                                         | AGATTTAAATTTAGGAAGACTGAATTA---AATTAAGATTTGATACATAGTAAATTA    | 988            |             |
| Qy                    | 2725                                                         | AATTTAATATTAACAATAAATAATTTATTTTACTTCAAAATCTTACTTAATATGATTAAT | 2784           |             |
| Db                    | 987                                                          | TATTCAGCTAATATTTGAGAAACTGTGTTTCCGTGACTAAATTTCTAGTACATAAATGA  | 928            |             |
| Qy                    | 2785                                                         | CATTTTATTTTCTGAGGGAAGACATACACTTTTAAAGTGAAGTGAATTAAGT         | 2844           |             |
| Db                    | 927                                                          | TCATACTTATTCCTGTATTTATTAACATGGAATTAATTTTAAATATCTTTTATTCAG    | 868            |             |
| Qy                    | 2845                                                         | TTATTCACCTAAATTAATTAATTTTAAAGTTTACATATTAAGATGAATGAATCTAAGT   | 2904           |             |
| Db                    | 867                                                          | TGAAATTCGTGCTCAGTTTCAACTGATTTTCTCCATTCCTAAAGTGCAGATTAATAT    | 808            |             |
| Qy                    | 2905                                                         | TATATGTTATGTTAATAAAGTTTAAATTTTTCGATGTCATACAGCTTTATATT        | 2964           |             |
| Db                    | 807                                                          | GGCAGAAGATGTTTTTTCATGTGTTATTAACAAGAGATTAATGTCAGTTCTATTAAT    | 748            |             |
| Qy                    | 2965                                                         | CATAGATTTATTCCTTTTAAAGATGATCAATGAATCAAGCTCACCTTGATCTGTAACA   | 3024           |             |
| Db                    | 747                                                          | TGTAGATTTATTTCTTTTATGAAGTGAATGAATGATCAAGCTCACCTTGATCTGTAACA  | 688            |             |
| Qy                    | 3025                                                         | AATACGTTTGTGACCTTGACAGACAGGGTTTAAACCTCGACAGCAGAGATTCATGTT    | 3084           |             |
| Db                    | 687                                                          | AATACGTTTGTGACCTTGACAGACAGGGTTTAAACCTCGACAGCAGAGATTCATGTT    | 628            |             |
| Qy                    | 3085                                                         | GGAGCAAGAGCCAAATCACAGATCCGACAGCACTTGTCTCATCAAGTTGGAATTAATA   | 3144           |             |
| Db                    | 627                                                          | GGAGCAAGAGCCAAATCACAGATCCGACAGCACTTGTCTCATCA--GTGGAATTAATA   | 570            |             |
| Qy                    | 3145                                                         | AGCCACTTGGAAATACAGTATTAAGATTCATCTGTGTGGCAAGTTGTCTCTCAGACTGG  | 3204           |             |
| Db                    | 569                                                          | AGCCACTTGGAAATACAGTATTAAGATTCATCTGTGTGGCAAGTTGTCTCTCAGACAGTG | 510            |             |
| Qy                    | 3205                                                         | CAGGCAATTAACGTTTGGCTTGGGTTAATCAAAAGAAAAAAGAAATTAAGAAAGAAAGT  | 3264           |             |
| Db                    | 509                                                          | CAGGCAATTAATTTTGGCTTGGGTTAATCAAAAGC---AAAGTAAAGAAAGAAAT      | 455            |             |

|          |                                                                           |                                                           |      |
|----------|---------------------------------------------------------------------------|-----------------------------------------------------------|------|
| QY       | 3265                                                                      | AAGAACAGAGGAAAAGATGGATTGATTTTAAACATGCAGAAAACGCAATCGTGT    | 3322 |
| DB       | 454                                                                       | AAGAACAGAGGAAAAGATGGATTGATTTTAAATCATGCAGAAAACGCAATCTATGTT | 395  |
| QY       | 3325                                                                      | TATATTTACCTATTTATGCTGATTTGTTG                             | 3352 |
| DB       | 394                                                                       | TATATTTACCTGTTTATGCTGCTATCTG                              | 367  |
| RESULT 8 |                                                                           |                                                           |      |
| AAZ50113 |                                                                           |                                                           |      |
| ID       | AAZ50113                                                                  | standard; DNA; 396 BP.                                    |      |
| AC       | AAZ50113;                                                                 |                                                           |      |
| XX       |                                                                           |                                                           |      |
| DT       | 04-MAY-2000                                                               | (first entry)                                             |      |
| XX       |                                                                           |                                                           |      |
| DE       | Mouse growth differentiation factor-8 promoter element.                   |                                                           |      |
| KW       | Growth differentiation factor gene promoter; GDF; gene therapy;           |                                                           |      |
| KW       | tissue specific gene expression; cancer; AIDS; cachexia; mouse;           |                                                           |      |
| KW       | muscle associated disorder; muscular dystrophy; spinal cord injury;       |                                                           |      |
| KW       | traumatic injury; congestive obstructive pulmonary disease; obesity;      |                                                           |      |
| KW       | diabetes; cytostatic; immunomodulator; antidiabetic; anorectic; cardiant; |                                                           |      |
| KW       | de.                                                                       |                                                           |      |
| OS       | Mus musculus.                                                             |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PH       | Key                                                                       | Location/Qualifiers                                       |      |
| FT       | misc_feature                                                              | 83..240                                                   |      |
| FT       |                                                                           | /*tag= a                                                  |      |
| FT       |                                                                           | /note="Portion of GDF-8 promoter element claimed as SEQ   |      |
| FT       |                                                                           | ID NO:7"                                                  |      |
| FT       |                                                                           | 91..96                                                    |      |
| FT       | misc_binding                                                              | /*tag= c                                                  |      |
| FT       |                                                                           | /bound_moiety= "Transcription factor"                     |      |
| FT       |                                                                           | /note="Functions as a regulatory region"                  |      |
| FT       |                                                                           | 145..150                                                  |      |
| FT       | misc_binding                                                              | /*tag= d                                                  |      |
| FT       |                                                                           | /bound_moiety= "Transcription factor"                     |      |
| FT       |                                                                           | /note="Functions as a regulatory region"                  |      |
| FT       |                                                                           | 165..170                                                  |      |
| FT       | misc_binding                                                              | /*tag= e                                                  |      |
| FT       |                                                                           | /bound_moiety= "Transcription factor"                     |      |
| FT       |                                                                           | /note="Functions as a regulatory region"                  |      |
| FT       |                                                                           | 393..236                                                  |      |
| FT       | TATA_signal                                                               | /*tag= b                                                  |      |
| PN       | WO200004051-A2.                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PD       | 27-JUN-2000.                                                              |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PF       | 15-JUL-1999;                                                              | 99WC-US016026.                                            |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PR       | 15-JUL-1998;                                                              | 98US-0092865P.                                            |      |
| XX       |                                                                           |                                                           |      |
| PR       | 08-MAR-1999;                                                              | 99US-0123270P.                                            |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PA       | (META-) METAMORPHIX INC.                                                  |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PI       | Liang L;                                                                  |                                                           |      |
| XX       |                                                                           |                                                           |      |
| DR       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| WPI      | 2000-182405/16.                                                           |                                                           |      |
| PT       | Novel promoter sequence for tissue specific gene expression in gene       |                                                           |      |
| PT       | therapy, for treating muscle associated disorders, e.g. muscular          |                                                           |      |
| PT       | dystrophy.                                                                |                                                           |      |
| XX       |                                                                           |                                                           |      |
| XX       |                                                                           |                                                           |      |
| PS       | Claim 5; Fig 7; 40pp; English.                                            |                                                           |      |
| CC       | The patent discloses the use of growth differentiation factor (GDF) gene  |                                                           |      |
| CC       | promoters for tissue specific gene expression in gene therapy. These      |                                                           |      |
| CC       | elements are located upstream of the 5' end of a GDF gene. GDF promoters  |                                                           |      |

CC ensure proper binding and activation of RNA polymerase and influence  
CC transcription levels. They are used for muscle specific expression of a  
CC gene by transfecting it into a muscle cell and thus treatment of muscle  
CC associated disorders e.g. cancer, muscular dystrophy, spinal cord and  
CC traumatic injury, congestive obstructive pulmonary disease, AIDS,  
CC cachexia, and obesity or its related disorders (e.g. diabetes) and  
CC disorders related to abnormal proliferation of adipocytes by gene  
CC therapy. The present sequence is mouse GDF-8 promoter element isolated by  
CC screening a mouse GDF-8 genomic clone. This sequence shows a high level  
CC of homology with human, pig and chicken GDF-8 promoter elements  
XX

SO Sequence 396 BP; 131 A; 70 C; 80 G; 115 T; 0 U; 0 Other;

Query Match 7.7%; Score 259.4; DB 3; Length 396;  
Best Local Similarity 82.3%; Pred. No. 3.1e-41;  
Matches 312; Conservative 0; Mismatches 61; Indels 6; Gaps 1;

OY 2920 ATTAAGTTTAAATTTTTCGATGTCACATACAGCTTATTTATTCATAGATTATTCCT 2979  
DB 18 ACACAGACTTCATTTATTCATCAATATGTCATATATCTTCATATGATTTGGGATTTATTTCA 77  
OY 2980 TTTAAGAGTATGTAATGAATCAGCTCACCTTGTACGTGTAACAAATATCTTTGGTGA 3039  
DB 78 TTTATGAAGTATGTAATGAATCAGCTTGTCTGCACTGTAACAAATATCTGCTTGGTGA 137  
OY 3040 CTTGTGACAGACAGGGTTTAACTCTGACAGCAGATTCATTTGTGACAGCAAGCCAT 3099  
DB 138 CTTGTGACAGACAGGGTTTAACTCTGACAGCAGATTCATTTGTGACAGCAAGCCAT 197  
OY 3100 CACAGATCCGACGACACTTGTCTCATCAAAAGTTGAAATATTAAGCCACTTGGAAATAC 3159  
DB 198 CATGATCTTCAACGACACTTGTCTCTTAAGTTGAATATTAAGCACTTGGAAATAC 257  
OY 3160 AGTATTAAGTATCTGCTGTGCAAGTATGCTCTGACATGGGACAGCAATACCTT 3219  
DB 258 AGTATTAAGTATCTGCTGTGCAAGTATGCTCTGACATGGGACAGCAATACCTT 317  
OY 3220 GCGTTGGCTTACTCAAAAGCAAAAGAAAGTAAAGAGAGATTAAGCAAGGAAAA 3279  
DB 318 CACTTGGCATTAATCAAAAGCAAAAGAAAGTAAAGAGAGATTAAGCAAGGAAAA 371  
OY 3280 GATTGTATTAATTTTAAAA 3298  
DB 372 GATTGTCTGATTTTAAAA 390

RESULT 9  
ADH11572  
ID ADH11572 standard; cDNA; 2823 BP.

XX ADH11572;  
XX  
XX 11-MAR-2004 (first entry)  
XX  
XX Human bone morphogenic protein (BMP) polynucleotide #21.  
XX  
XX Human; bone morphogenic protein; BMP; gene; ss; weight gain;  
KW appetite suppression; fat mass reduction; cell sensitivity;  
KW glucose uptake; diabetes; insulin resistance; hyperglycaemia;  
KW hyperextension; coronary artery disease; renal failure; neuropathy;  
KW metabolic disorder; glucose metabolism disorder; endocrine disorder;  
KW obesity; weight loss; liver disorder; cartilage growth disorder;  
KW bone growth disorder; inflammation; aberrant cell growth; liver cancer.  
XX  
XX Homo sapiens.  
XX  
XX US200324501-A1.  
XX  
XX 04-DEC-2003.  
XX  
XX 14-FEB-2003; 2003US-00366345.  
XX  
XX 17-MAR-2000; 2000US-0190067P.  
XX  
XX PR

PR 16-MAR-2001; 2001US-00809269.  
PR 23-MAR-2001; 2001WO-US009229.  
PR 17-JAN-2002; 2002US-0348621P.  
PR 22-JAN-2002; 2002US-0349356P.  
PR 28-JAN-2002; 2002US-0351520P.  
PR 06-FEB-2002; 2002US-0354265P.  
PR 15-FEB-2002; 2002US-0356749P.  
PR 16-JAN-2003; 2003US-00345236.  
XX  
XX (YOUNG) YOUNG P. E.  
XX (RUBEN) RUBEN S. M.  
XX  
XX Young PE, Ruben SM;  
XX  
XX WPI: 2004-022075/02.  
XX P-PDB; ADH11595.  
XX

PT New bone morphogenic protein polypeptides and polynucleotides, useful for  
PT diagnosing, preventing, treating or ameliorating a medical condition,  
PT e.g. diabetes, dyslipidemia, hypertension, coronary artery disease or  
PT neuropathy.  
XX

PS Example 1; SEQ ID NO 27; 224bp; English.

XX The invention relates to human bone morphogenic protein (BMP)  
XX polypeptides and the polynucleotides encoding them. The invention also  
XX relates to a method for limiting weight gain, suppressing appetite or  
XX reducing fat mass, comprising administering to a mammalian subject a  
XX therapeutic amount of a BMP polypeptide, and a method for increasing the  
XX sensitivity of a cell to insulin or increasing glucose uptake by a cell,  
XX comprising contacting the cell with a BMP polypeptide. The BMP  
XX polypeptides and polynucleotides are useful for diagnosing a pathological  
XX condition or a susceptibility to a pathological condition in a subject or  
XX for preventing, treating or ameliorating a medical condition, e.g.  
XX diabetes, insulin resistance, hyperglycemia, hypertension, coronary  
XX artery disease, renal failure, neuropathy, metabolic disorders, glucose  
XX metabolism disorder, endocrine disorders, obesity, weight loss, liver  
XX disorders, cartilage and bone growth disorders, inflammation or aberrant  
XX cell growth such as liver cancer. The BMP polypeptides and  
XX polynucleotides are also useful for regulating nutritional partitioning,  
XX limiting weight gain, suppressing appetite, reducing fat mass, increasing  
XX the sensitivity of a cell to insulin or increasing glucose uptake by a  
XX cell. This sequence represents a human BMP polynucleotide of the  
XX invention.  
XX

SEQ Sequence 2823 BP; 978 A; 457 C; 497 G; 891 T; 0 U; 0 Other;

Query Match 5.6%; Score 190; DB 12; Length 2823;  
Best Local Similarity 91.0%; Pred. No. 2e-27;  
Matches 202; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 3168 AGATTCACCTGTGTGGCAAGTTGCTCTCAGACATGGGACAGCATTAAGTTGGCTTGGC 3227  
DB 1 AGATTCACCTGTGTGGCAAGTTGCTCTCAGACATGGTATTAAGTTTCTTGGC 60  
OY 3228 GTTACTCAAAAGCAAAAGAAAGTAAAGAGAAAGTAAAGCAAGGAAAAAGTTGAT 3287  
DB 61 ATTACTCAAAAGCAAAAGAAAGTAAAGAGAAAGCAAGCAAGAAAAAGTTATAT 120  
OY 3388 TGATTTTAAAAACATGCAAAAGTCAAAATCTCTGTTTATTTATTAACCTATTTATGCTGAT 3347  
DB 121 TGATTTTAAAAACATGCAAAAGTCAAAATCTCTGTTTATTTATTAACCTGTTATGCTGAT 180  
OY 3348 TGTTCCTGCGCCCATGATGATCTGAATGAGACAGGACGAGAA 3389  
DB 181 TGTTCCTGCTCCAGTGAATTAATGAGAACAGTGACGACAAA 222

RESULT 10  
AAFS8663  
ID AAFS8663 standard; DNA; 200 BP.  
XX  
XX AAFS8663;  
XX  
XX AC

XX 27-APR-2001 (first entry)

DE Murine myostatin gene promoter fragment.

XX Mouse; myostatin; promoter; cyostatic; anti-HIV; neuroprotective;  
 XX immunomodulator; cancer; muscular dystrophy; spinal cord injury;  
 KW neurodegenerative disorder; congestive obstructive pulmonary disease;  
 KW COPD; amyotrophic lateral sclerosis; acquired immunodeficiency syndrome;  
 KW AIDS; cachexia; ageing; ds.

XX Mus musculus.

XX EP1072680-A1.

XX 31-JAN-2001.

XX 27-JUL-2000; 2000EP-00306396.

XX 30-JUL-1999; 99US-0146540P.

XX (PRIZ ) PRIZER PROD INC.

XX Findly RC;

XX WPI; 2001-170964/18.

XX Novel myostatin gene promoter for regulating expression of heterologous  
 PT genes in cells or animals, for identifying compounds that inhibit its  
 PT activity or expression, which are useful for treating muscle disorders.

PS Claim 3; Page 13; 24pp; English.

XX The present sequence is part of an isolated myostatin gene promoter.  
 CC Regulating the transcription activities or expression of the promoter is  
 CC useful for treating muscle associated disorders such as cancer, muscular  
 CC dystrophy, spinal cord injury, neurodegenerative disorders, traumatic  
 CC injury, congestive obstructive pulmonary disease (COPD), amyotrophic  
 CC lateral sclerosis, acquired immunodeficiency syndrome (AIDS), cachexia or  
 CC ageing. The promoter is useful for modulating the expression of the  
 CC myosin gene for producing animal food products having increased muscle  
 CC and protein content and reduced fat and cholesterol content, for  
 CC regulating expression of a heterologous gene in cells or animals, to  
 CC engineer host cells, to screen for compounds that inactivate or inhibit  
 CC its transcription and expression, for inhibiting its expression in cells  
 CC for the promotion of muscle growth, for diagnostic evaluation, genetic  
 CC testing and prognosis of a disease or disorder associated with myostatin  
 CC expression

XX Sequence 200 BP; 57 A; 44 C; 48 G; 51 T; 0 U; 0 Other;

XX Query Match 5.1%; Score 174.4; DB 4; Length 200;

XX Best Local Similarity 92.0%; Pred. No. 1.3e-24;

XX Matches 184; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2990 AGTCAATGATCAGTCACTTGTGACGTAACAAATCTGTTGGTACTTGTGACG 3049

DB 1 AGTCAATGATCAGTCACTTGTGACGTAACAAATCTGTTGGTACTTGTGACG 60

QY 3050 ACAGGATTTAACTTGTGACGAGGATTCATTGTGAGCAGAGCAATCAAGATCC 3109

DB 61 ACAGGATTTAACTTGTGACGAGGATTCATTGTGAGCAGAGCAATCAAGATCC 120

QY 3110 GACGACACTTGTCTATCAAAAGTTGAATATTAAGCCACTTGGAAATCAATATTAAG 3169

DB 121 GACGACACTTGTCTATCAAAAGTTGAATATTAAGCCACTTGGAAATCAATATTAAG 180

QY 3170 ATTCACTGTTGGCAAGTT 3189

DB 181 ACTCCCTGGCGTGGCAGGTT 200

RESULT 11

AAZ50115  
 ID AAZ50115 standard; DNA; 156 BP.

XX AAZ50115;

DT 04-MAY-2000 (first entry)

XX Pig growth differentiation factor-8 promoter element.

XX Growth differentiation factor gene promoter; GDF; gene therapy;  
 KW tissue specific gene expression; cancer; AIDS; cachexia; mouse;  
 KW muscle associated disorder; muscular dystrophy; spinal cord injury;  
 KW traumatic injury; congestive obstructive pulmonary disease; obesity;  
 KW diabetes; cyostatic; immunomodulator; antidiabetic; anorectic; cardiant;  
 ds.

XX Sus scrofa.

XX Key Location/Qualifiers

FT misc\_binding 9..14  
 FT /tag= a  
 FT /bound\_molecy= "Transcription factor"

FT /note= "Functions as a regulatory region"

FT misc\_binding 63..68  
 FT /tag= b  
 FT /bound\_molecy= "Transcription factor"

FT /note= "Functions as a regulatory region"

FT misc\_binding 83..88  
 FT /tag= c  
 FT /bound\_molecy= "Transcription factor"

FT /note= "Functions as a regulatory region"

FT TATA\_signal 152..156  
 FT /tag= d

XX WO200004051-A2.

XX 27-JAN-2000.

XX 15-JUL-1999; 99WO-US016026.

XX 15-JUL-1998; 98US-0092865P.

XX 08-MAR-1999; 99US-0132270P.

XX (META-) METAMORPHIX INC.

XX Liang L;

XX WPI; 2000-182405/16.

XX Novel promoter sequence for tissue specific gene expression in gene  
 PT therapy, for treating muscle associated disorders, e.g. muscular  
 PT dystrophy.

PS Claim 5; Fig 8; 40pp; English.

XX The patent discloses the use of growth differentiation factor (GDF) gene  
 CC promoters for tissue specific gene expression in gene therapy. These  
 CC elements are located upstream of the 5' end of a GDF gene. GDF promoters  
 CC ensure proper binding and activation of RNA polymerase and influence  
 CC transcription levels. They are used for muscle specific expression of a  
 CC gene by transfecting it into a muscle cell and thus treatment of muscle  
 CC associated disorders e.g. cancer, muscular dystrophy, spinal cord and  
 CC traumatic injury, congestive obstructive pulmonary disease, AIDS,  
 CC cachexia, and obesity or its related disorders (e.g. diabetes) and  
 CC disorders related to abnormal proliferation of adipocytes by gene  
 CC therapy. The present sequence is pig GDF-8 promoter element isolated by  
 CC screening a pig GDF-8 genomic clone obtained from GenBank Accession  
 CC numbers AJ133580 and AF093798. This sequence shows a high level of  
 CC homology with human, mouse and chicken GDF-8 promoter elements

XX Sequence 156 BP; 50 A; 31 C; 34 G; 41 T; 0 U; 0 Other;

XX Query Match 4.2%; Score 141.8; DB 3; Length 156;



Best Local Similarity 98.6%; Pred. No. 3e-18;  
Matches 143; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2985 GAAGTAGCAATGATGAGCTACCTTGACTGTAACAAATAGTTGGTGACTTGT 3044  
Dd 1 GAAGTAGCAATGATGAGCTACCTTGACTGTAACAAATAGTTGGTGACTTGT 60

QY 3045 GACAGACAGGGTTTAACTCTGACAGGAGATTGTTGGAGCAGACCAATCAGC 3104  
Dd 61 GACAGACAGGGTTTAACTCTGACAGGAGATTGTTGGAGCAGACCAATCAGC 120

QY 3105 ATCCGAGACACTTGTCTCATCA 3129  
Dd 121 ATCCGAGACACTTGTCTCATCA 145

## RESULT 12

AAV89102 ID AAV89102 standard; cDNA; 336 BP.

AAV89102; AC

DT 15-FEB-1999 (first entry)

DE EST clone BV995.

XX Human; secreted protein; expressed sequence tag; EST; haematopoiesis;

XX tissue growth; actinin; inhibin; chemotaxis; chemokinesis; haemostatic;

XX receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;

XX gene therapy; ss.

XX Homo sapiens.

XX MO9845436-A2.

XX 15-OCT-1998.

XX 10-APR-1998; 98WO-US006955.

XX 10-APR-1997; 97US-00838821.

XX (GENY) GENETICS INST INC.

XX Jacobs K, Mccoy JM, Lavalie ER, Racie LA, Merberg D, Treacy M;

XX Spaulding V, Agostino MJ;

XX WPI; 1999-070077/06.

XX Claim 1; Page 111; 618pp; English.

XX The present sequence represents a human expressed sequence tag (EST). The  
XX polynucleotide, which is a secreted EST, and the encoded protein are  
XX predicted to have useful biological activities which would make them  
XX suitable for treating, preventing or ameliorating medical conditions in  
XX humans and animals, although no supporting data is given. Suggested  
XX activities include nutritional activity, immune stimulating or  
XX suppressing activity, haematopoiesis regulating activity, tissue growth  
XX activity, actinin/inhibin activity, chemotactic/chemokinetic activity,  
XX haemostatic and thrombolytic activity, receptor/ligand activity, anti-  
XX inflammatory activity, cadherin/tumour invasion suppressor activity,  
XX tumour inhibition activity. The polynucleotide may also be useful for  
XX gene therapy

XX Sequence 336 BP; 136 A; 52 C; 65 G; 83 T; 0 U; 0 Other;

XX Query Match 4.0%; Score 136.2; DB 2; Length 336;

XX Best Local Similarity 86.7%; Pred. No. 4.5e-17;

XX Matches 150; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 3217 TTGGCTTGCGCTTACTCAAAAGCAAAAGAAAGTAAAGAGAGTAGAACAAGGCA 3276  
Dd 4 TTGGCTTGCTTCAATGCGCTTAAAGCAAAAGAAAGTAAAGAGAGAGCAAGCAAA 63

QY 3277 AAAGATTGATTTGATTTTAAACCATGCAAAATCTCTGTTATTTACTCTA 3336  
Dd 64 AAAGATTGATTTGATTTTAAACCATGCAAAATCTCTGTTATTTACTCTG 123

QY 3337 TTATGCTGATTTGCTGCGCCAGTGGATCTGATGAGAGAGAGAGAGCA 3389  
Dd 124 TTATGCTGATTTGCTGCGCCAGTGGATCTGATGAGAGAGAGAGAGCA 176

## RESULT 13

AAV24415 ID AAV24415 standard; cDNA; 1195 BP.

AAV24415; AC

DT 07-JUN-1999 (first entry)

DE Bovine myostatin cDNA.

XX Myostatin; cattle; bovine; transforming growth factor beta;

XX double muscling; muscle hyperplasia; transgenic animal; ss.

XX Bos taurus.

XX Key Location/Qualifiers

XX CDS 46..1173

XX mutation 863..873

XX /\*tag= b

XX /note= "deleted in mutant gene (nt821(del11) mutation)"

XX MO9902667-A1.

XX 21-JAN-1999.

XX 14-JUL-1998; 98WO-IB001197.

XX 14-JUL-1997; 97US-00891789.

XX 15-JAN-1998; 98US-00007761.

XX (UNIV) UNIV LIBGE.

XX Grobet L, Georges M, Poncelet D;

XX WPI; 1999-120869/10.

XX P-PSDB; AAV97884.

XX Increasing muscle mass in mammals - by decreasing myostatin expression.

XX Claim 7; Page 54; 75pp; English.

XX This is the nucleotide sequence of a cDNA clone encoding bovine myostatin  
XX (see AAV97884), a member of the transforming growth factor beta  
XX superfamily. A mutant gene (see AAV24415) in which the coding sequence  
XX lacks an 11 bp consecutive sequence (see AAV24421) has also been  
XX sequenced. Cattle of the Belgian Blue breed homozygous for the mutant  
XX gene are double-muscling. A new method of increasing muscle mass of a  
XX mammal having myostatin-expressing muscle cells, comprises administration  
XX of a nucleic acid molecule substantially complementary to at least a  
XX portion of mRNA encoding myostatin and of sufficient length to reduce  
XX myostatin expression and thus increase muscle mass. A ribozyme may also  
XX be used. Also claimed are: a method for determining muscular hyperplasia  
XX (MH) in a mammal using primers based upstream and downstream of the  
XX mutation; a diagnostic kit for determining the genotype of a sample of  
XX genetic material; a method for determining MH in a mammal; a method for  
XX determining double muscling in a bovine animal; a method for determining  
XX the myostatin genotype of an animal; purified myostatin; isolated nucleic  
XX acids; a microbial host cell; a probe based on the myostatin gene  
XX mutation; transgenic mammals having MH phenotype; a myostatin knockout

CC animal; and a transgenic bovine having a gene encoding active myostatin,  
 CC and a heterologous nucleotide sequence antisense to that gene, and  
 CC optionally further containing a gene encoding a nucleic acid sequence  
 CC with ribozyme activity in transcriptional association with the antisense  
 CC sequence. Primers are preferably based on genomic bovine myostatin DNA  
 CC (see AAX24464) and human myostatin cDNA (see AAX24418)  
 XX

SO Sequence 1195 BP; 379 A; 250 C; 261 G; 305 T; 0 U; 0 Other;

Query Match 3.8%; Score 127.6; DB 2; Length 1195;  
 Best Local Similarity 97.0%; Pred. No. 2.9e-15;  
 Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3257 GAAGAGTAAGAAAGAGGAAAGATGTGATGATTTAAACATGCAAAACTGCAAA 3316  
 Db 2 GGAAGAAATPAGAACAGGAAAGATGTGATGATTTAAACATGCAAAACTGCAAA 61

QY 3317 TCTGCTTATTTATTTACTTATTTATGCTGATTTGTCGCCCACTGATCTGATGAGA 3376  
 Db 62 TCTGCTTATTTATTTACTTATTTATGCTGATTTGTCGCCCACTGATCTGATGAGA 121

QY 3377 ACAGCGACGACGAG 3390  
 Db 122 ACAGCGACGACGAG 135

RESULT 14  
 ADS31200  
 ID ADS31200 standard; DNA; 653 BP.  
 XX  
 AC ADS31200;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Human genome high complexity repeat found in the HIRA gene #233.  
 XX  
 KW Human; ds;  
 KW histone cell cycle regulation defective; S. cerevisiae homologue A; HIRA;  
 KW high complexity repeat; in situ hybridisation; Southern blot; HIRA;  
 KW chromosome breakpoint; inherited genetic disease; neoplastic disorder;  
 KW chromosome 22; DiGeorge syndrome; Velo-Cardio-facial syndrome.  
 XX  
 OS Homo sapiens.  
 XX  
 EN US2003224356-A1.  
 XX  
 PD 04-DEC-2003.  
 XX  
 PF 14-MAY-2001; 2001US-00854867.  
 XX  
 PR 16-MAY-2000; 2000US-00573080.  
 XX  
 PA (KNOOL/) KNOOL J H M.  
 PA (ROGA/) ROGA P K.  
 XX  
 PI KNOOL JHM, Rogan PK;  
 XX  
 DR WPI; 2002-062378/08.  
 XX  
 PT Single copy genomic hybridization probes for detecting specific nucleic  
 PT acid sequences in sample by in situ hybridization useful for detection of  
 PT acquired or inherited genetic diseases.  
 XX  
 PS Example 1; SEQ ID NO 233; 30pp; English.  
 XX  
 CC The invention relates to a nucleic acid hybridisation probe comprising a  
 CC labelled, single copy nucleic acid of at least 50 nucleotides, which  
 CC will hybridise to a deduced single copy sequence interval in target  
 CC nucleic acid (TNA) of known sequence. The single copy sequence is deduced  
 CC by comparing the target nucleic acid (e.g. a disease causing gene) with a  
 CC collection of high and low complexity repeat sequences as found in the  
 CC genome of the organism from containing the target nucleic acid. The probe  
 CC is generated by PCR on the target sequence. The probe is essentially free

CC of blocking nucleic acid sequences which will hybridise to repeat  
 CC sequences within the genome of which the TNA is a part, and is labelled  
 CC with a label selected from fluorochrome-responsive labels, fluorochromes,  
 CC calorimetric chemical, conjugated proteins, antibodies, antigens and  
 CC their mixtures. The probe is useful in a hybridisation method, where the  
 CC hybridisation method is from in situ hybridisation, Southern blot, and  
 CC other methods in which nucleic acid is immobilised, where the method  
 CC further comprises selecting a single copy nucleic acid which will  
 CC hybridise to a duplilon or triplicon sequence domain. The probe is useful  
 CC for determining the existence of previously unknown repeat sequence  
 CC families in a genome. The method comprises reacting a labelled probe with  
 CC the genome, causing the probe to hybridise and ascertaining if the probe  
 CC locations as a determination of new repeat sequence family, where the  
 CC determining step comprises selecting the single copy sequence from a  
 CC duplilon or triplicon sequence domain. The probe is useful for  
 CC determining a chromosome breakpoint and is useful in the field for  
 CC cytogenetics and molecular genetics for determining the presence of  
 CC specific nucleic acid sequences in a sample of eukaryotic origin, e.g.  
 CC the probes may be used to analyse specific chromosomal locations by in  
 CC situ hybridisation as a detection of genetic or neoplastic disorders.  
 CC diseases especially for detection of genetic or neoplastic disorders.  
 CC Unlike prior art techniques, the probe permits more precise chromosomal  
 CC breakpoint determinations by in situ hybridisation. The genomic sequence  
 CC comprising the human HIRA gene (histone cell cycle regulation defective,  
 CC S. cerevisiae, homologue A) was analysed for single copy sequence  
 CC intervals for use as probes of the invention. HIRA is located on  
 CC chromosome 22 as a duplicate, deletions of 1 copy lead to DiGeorge and  
 CC Velo-Cardio-facial syndromes. The present sequence is a high complexity  
 CC repeat found within the human genome used to analyse the HIRA gene for  
 CC repeat regions. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from USPTO at [seqdata.uspto.gov/sequence.html?docID=20030224356](http://seqdata.uspto.gov/sequence.html?docID=20030224356).

SO Sequence 653 BP; 200 A; 139 C; 132 G; 176 T; 0 U; 6 Other;

Query Match 3.7%; Score 126.2; DB 7; Length 653;  
 Best Local Similarity 70.9%; Pred. No. 4.7e-15;  
 Matches 222; Conservative 1; Mismatches 81; Indels 9; Gaps 4;

QY 119 AGCTGACCTCTATTTATTTACAGTGTGTTATGTTTACCAATCAGTCCGCAACA- 177  
 Db 2 AGTGTATCTCTATTTATTTACAGTGTGTTATGTTTACCAATCAGTCCGCAACA- 61

QY 178 GTGATTCCTGAACCACTGCCCTAGGGAGACTACAGGTTAGATCCCGTCAAGCCTCTG 237  
 Db 62 GCGATTAAGTCAACATCGCTCTAGAGGAATACAGATTAGTTCCGCAAGCCTCTG 121

QY 238 TC--ACGTTTTTGTAAACAATCAATTAATTAACCTGTTTGTGTCATTTCTGTTTA 294  
 Db 122 TCACAACATTTTCAATCAACGATCAATTAATTAACCTGTTTGTGTTTCTGTTTA 181

QY 295 AATATCTTTATTTATTAACGTAATCTGTAATCTTCAACATTTGTTCAACCAAGG 354  
 Db 182 AGACNNC--TTATTTATTTATTAATTTGTTATTTATTAACCTGTAATCTGTAAG-- 238

QY 355 CCTATTAATGGAAGCCCTGAATGAAGTTACATTAACACACATTTGTTTATGAGGA 414  
 Db 239 --CACTTAATCAATGCTGTAATGAAGTTATTAACACACATTTTCTCATTAAGGA 296

QY 415 AATATTTTCTCTC 427  
 Db 297 CATCAAGCTTC 309

RESULT 15  
 AA206449  
 ID AA206449 standard; DNA; 2742 BP.  
 XX  
 AC AA206449;  
 XX  
 DT 08-DEC-1999 (first entry)  
 XX



**THIS PAGE BLANK (USPTO)**

354 אבן עזרא על ספר שמות פרק יא

Db 471 CAGACATTAACCTGAGGCTGAATGATGCTTATGACACA---TGACTTTTTCATGAG 527  
Qy 414 AAAATTTTCTCTGATGCTGCGACAGGCTTCTGTTAAATTTGGACAAATATACA 473  
Db 528 AACCTTTTCCCTTAGGATATACAGGCTT-----TTAAATTTGTGTAAATTTACCA 582  
Qy 474 TAAATGAAATGATATATTTAATGATTTTAACTGATGTTCAAGTTCAGTGGCATTAAGTA 533  
Db 583 ACATTTAGCA-----TCTTAACCATTTTAACTTTAGTTTCAAGTTTGGATTTAGCA 633  
Qy 534 CACTTACCTTGTGATGAACTATGATCAACATTCCTCTAGAACTTTTGTATCTTCTCG 593  
Db 634 CATTCACACTGTGTGTATACATACACACATTCATCTTGAGAAATTTTTCATCTGCCA 693  
Qy 594 AATTGAAAATCTGATCTTATTTGACAGTAGCTTTCCCTCATCACAGGACCTTCTCTC 653  
Db 694 GACTG-AAAATCTGTATCTATACACAGTAACTACCTCA-----GTGCTTACC 743  
Qy 654 CAGCCCCCGGACACACATCTTCTTCAATGACAGTCACTCTGTGCTAGGAACA--- 710  
Db 744 CAGTCCCTGGCAACACATGCTACTTTCATGTCAGCTTCTCTGTGATTGAAACATAG 803  
Qy 711 -----CAGCCCTTCAACACTACGCTTGGGGGCACTGT---AAGCAACAGATC 756  
Db 804 GAACACACGACGACGTCAGACATATGCTTGGGGGCACTTTTAAAGCAAAATCAAT 863  
Qy 757 ACTCCATCCGCGACCAATATGACACAAATATATTAAGCATGTGGCATATGCAATGC 816  
Db 864 AAGAGACCAATATTAATAAGAGACAAATATGTGAAACATGTGCATTAATATACGG 923  
Qy 817 AAAAAGGGTGTGCT--AAGTATAGGGGCTGAAC---AAGGACAGAAATGACTAGT 871  
Db 924 AAAAAGGAAATTTTGTATATGATATAGTAGAGCTGAAACAAAAGGCGAACCTGCTTGT 983  
Qy 872 TGACCTCAGCTGGGATCTGTGTGTGG--AAGCTCAAAATTTTCATTTGTGTGAT 929  
Db 984 TGACCTCATCTGGGAACCTGTGCTCAGATAGACATCAAAATTTTGTGCGCTGTGAT 1043  
Qy 930 ACGCAAAATGCTTATTAAGACATGTAGATTTGATTTAGAGTTAGATTAATCTCAG 989  
Db 1044 GCGACGATGACTGAAAAA---TGCTAGGAATTTGATTTCAATTAATATTTAGC 1099  
Qy 990 CAAGCATTAATGTGCAAGACGAGGATCATGATTAAGACATGACAT--GTGAAA 1047  
Db 1100 AAGTAGGCAATTTTGTATATACGAATCATTAATTAAGAAATGTCTGTAGCGGAAA 1159  
Qy 1048 TGATATCTTTTGTCTTTATTTCCAGGCACTAGAGAAAGCG-----T 1093  
Db 1160 TGACAACTTTGTTCATCTTTTCCAGGTGATTAAGATTAAGAGCTGGAACATGTCTGT 1219  
Qy 1094 CACAGGCTGCTTACACATTTTACTAGAGAGCTAGGCTATGTCACTGCG----- 1144  
Db 1220 AACCTGGCTGCTTGAATAATTTTACTTGCCTCACAGGCTTGAAGAGCTTTGTGAC 1279  
Qy 1145 ---TAGCTGGCAATTAACAAGTGAAGAGTTCATGTTCACTGTGAGGATTAATTAACA 1201  
Db 1280 TGATATTTGGACGCTATGACCTGAAAGCACTTCAAGTTCACTGTGAGCAATATTTTAA 1339  
Qy 1202 TAAATCTCAACCCCTCTGATGAAACAGAGCTAAAGTACTCAAGTACAGATTCAGTCA 1261  
Db 1340 TAAATCTCAACCCCTCTGATTAATAACAAGAGCAAGCACTCAAAATGCCAGTTATCAATTA 1399  
Qy 1282 CTTAATTAATGACAGGCACTGATCTCAACATTTTATGATATTTTGAATTTACATGCC 1321  
Db 1400 CTTAATTAATGACAGGCTGATTAATTCAGCAATTTTATGATCAATTAATTTATCC 1459  
Qy 1332 CAACCTGATAGGAAGCTGAAGTTAGAG---AAGTATCTCATTAATTAACA 1376  
Db 1460 CAACCTGATAGGAAGCTGAAGTTAGGAAGTTAAGTATCTCATTAATTAACA 1519  
Qy 1377 GT-----GGCAAACTGAGATCTGAACTCAGGTCTATCACTCAGAGACCTGAGATC 1428

Db 1520 GTTAGAAGTGCAAAAGTTGAGATTTGAATCTCAGGTCTATCTGACTCAGAGCTGAGTTC 1579  
Qy 1429 CCAATGCTACACAAATCTATATCAAGTTAAAGGAAAAAGATTTGATTTGCTCAGAG 1488  
Db 1580 TCAATTTCACTGCTATCAATTTCTAGACATTTTAAAAAAGTTTGACTTACTGGAAC 1639  
Qy 1489 TGTATAGGGGATATGTTACA---ATTATTAATTAACAAGATTTATATGTTAAAAATA 1545  
Db 1640 TGTATAGTCACTGTGTTAACAATGATCATTAACATTTGAAAGATTTTACATTTGAAAAATG 1699  
Qy 1546 AATTATCAAAACAAATTAATTTTAAAGCTGATCTTAATACGCTCCGAAACAAAGCT 1605  
Db 1700 AATTATCAAAACAAATTAATTTTAAAGCAAGTCTTAATATTTGCTCAATTAACAAGCT 1759  
Qy 1606 ATCTGAATCTTCAAGGCACTGTTGTGTGTGCTGTTTCTTAATCTTAAATGATGAG 1665  
Db 1760 ATCTGAATCTTCAAGGCACTGTTGTGTGTGCTGTTTCTTAATCTTAAATGATGAG 1818  
Qy 1666 CAATCTTAATGATTAATGTAAGGCA-TTTTTTCTCAAGAGATGATATACCTTTAAGA 1724  
Db 1819 CAATCTTAATGATTAATGTAAGGCA-TTTTTTCTCAAGAGATGATATACCTTTAAGA 1878  
Qy 1725 AATTGATGAAGAAATGATTAATTTTCAAGGCTATGATGATTTTATGATGACAGGCA 1784  
Db 1879 AATTGATGAAGAAATGATTAATTTTCAAGGCTATGATGATTTTATGATGACAGGCA 1938  
Qy 1785 GTAATTTAGTATCAATGTGGAATA---GTATGATCTTAATAATAATATTTGATATGA 1841  
Db 1939 GTAATTTAGTATCAATGTGGAATA---GTATGATCTTAATAATAATATTTGATATGA 1998  
Qy 1842 ACCACTGACTCTCTTGG-GGAAAAAGTAATGATTAATCTCTTTAGAGTCTTATGCT 1900  
Db 1999 GCACTGATCTCTTGGAAAAAAAGTAATGATGATTAATCTCTTGAATCTTATGCT 2058  
Qy 1901 TCCCAAAAGTAATGAAAAATTAATCTCTGAGCTGGAACAGCTTCTGTTCTG 1960  
Db 2059 TCCCAAAAGTAATGAAAAATTAATCTCTGAGCTGGAACAGCTTCTGTTCTG 2118  
Qy 1961 CTGCTATATTTGTTAGTTTATATGATTCATTTGATTAAGACTTGTGCTCCAAAG 2020  
Db 2119 CTGCTATATTTGTTAGTTTATATGATTCATTTGATTAAGACTTGTGCTCCAAAG 2178  
Qy 2021 CTAAGTTGAGATTTATCTCTTACAGAGGCACTTCAATTTAGAAACAAAAGCCCA 2080  
Db 2179 CTAAGTTGAGATTTATCTCTTACAGAGGCACTTCAATTTAGAAACAAAAGCCCTA 2238  
Qy 2081 TTTCTGCTCCCAACCTTACCCAAATCCCTGCAAGGTCTGCCCGGCTCAAAATGA 2140  
Db 2239 TTTCTGCTCCCAACCTTACCCAAATCCCTGCAAGGTCTGCCCGGCTCAAAATGA 2298  
Qy 2141 GAAACTGCAAAAGAACTAGAGGTGCGACAGTACTAGAAAGTAAAGATGACTA 2200  
Db 2299 AGAAATTTGGCAAAAGGCTGCAACA-----TA 2325  
Qy 2201 GCACTATCTGAAGAGCAAAAAATGGGACCTTCAATGATGTGTTCTTCCCTTCT 2260  
Db 2326 TCGAGATTTGGGAAACAAACAAAGGTCAACCTTATCATGATGCTCTTCTCTTAT 2385  
Qy 2281 GTGTTCAACAGCTCCGATATTAATTTAAGAGGATGATA-----ACTAATTTT 2312  
Db 2386 GTGCTCAATTAATTTGATTAATTTTATAGAAATGATGACATTTTATCTCTGCG 2445  
Qy 2313 TCTTTTACACTGGAAGGCTGAGGAAACCTTGTATCCCATCATTAATAATTCATCTTC 2372  
Db 2446 AATTTTACGCTGGAATCTGAGGAACTGATTAATCTGCGCATGCGATTAATAA 2505  
Qy 2373 TAAATCAATTAATGTTATTTAAG-----TCAAAATGCTGACAAATATCTCTTTTGA 2426  
Db 2506 TTTCAATCTTAATGTTATGATGAGATTTTCTACTGCGGCAATACCTCTTGTGAA 2565  
Qy 2427 TAAACAAAGAAAAACAATCTCTGAGCAATTAATTAATGCACTTTAGATAGAGT 2486  
Db 2566 TAAACAAATG-AAAAACACATCTTGTAGGTATGTTAATCTGATCTTTAGATTAAGAA- 2622



QY 2487 AACTTAATACAGTCAATGAACTGAATACATTTTCATATGATTAAGATAT---- 2542  
 Db 2623 ---ATTAATAGACCTCAGTCAAAAGTTGATTAATTTTCATATTAATAAGACATGAAA 2679  
 QY 2543 -TATTAAAGTAATTCATGACATTTTAATTA-AAGTGAATTTTCATATGCTT 2600  
 Db 2680 CTATGTAAAAATTAATTCATGACATATGTTATATTAACATGCTTCAATATTTTACT 2739  
 QY 2601 AAGAATTATTCAGGGAACAAGTTCTCAATTATACAGAAATCTTTACTATGATAC 2660  
 Db 2740 AAGAAATTTAGTCA-GAACAACAAGTTCTCAATTAATGATGAATTTCTCAACTAGTAA 2798  
 QY 2661 ACAGCTTTTCAATTAATGTC-TTCCGTAATTAATCTGATATTTTCAATTAACAAGATCA 2719  
 Db 2799 ATAAATCTTAATTTTAATTCAGGCTTCTCTATTTTATTTTCCATTTACTGACACTA 2858  
 QY 2720 AAAATTAATTAATTAACAATAAATTAATTTT-TACTTCAATGCTTACTTAATAGTA 2778  
 Db 2859 AAAATTAATTAATTAACAATAAATTAATTTTCTACTTCAATCTTGCCTAAACAATA 2918  
 QY 2779 TAAATCAATTTTATTTCTGAGGGAACAATACATCACTTTTATGATTAAGTAAAT 2838  
 Db 2919 TAAATCAATTTTATTTCTGAGGGAACAATATTC-ATATTTTAATTAATGATTAAT 2977  
 QY 2839 TAAATTAATTTCACTTAATTAATTAATTTTAAAGTTTCAATTAAGATGATTAAGATC 2898  
 Db 2978 TAAATTAATTTCACTTAATTAATTAATTAAGATGATGATTAAGATTAAGATTAAGATC 3037  
 QY 2899 TAAATTAATTTCACTTAATTAATTAATTTTAAATTTTCCATGATCAATCAAGCTTT 2958  
 Db 3038 ---AGTTTAATTAATTTCCCAACAATGATGATTTTGTATTTTCAATATCTTTT 3093  
 QY 2959 ATTAATCAATTAATTTCTTTTAAAGATGATCAATTAATCACTTCACTTCACTG 3018  
 Db 3094 ATTAATCAATTTTATTTTATTTTATTTTATGATGATTAATTAATTAATTAATTAATTAAT 3153  
 QY 3019 TAAATTAATTTCTTTTGTGATCTTGTGATCAAGACAGGTTTAACTTCAAGACAGAT 3078  
 Db 3154 TAAATTAATTTCTTTTGTGATCTTGTGATCAAGACAGGTTTAACTTCAAGACAGAT 3213  
 QY 3079 CATTTGAGACAGACCAATCAAGATCCGACAGACCTTGTCTCATCAAGTTGAAT 3138  
 Db 3214 CATTTGAGACAGACCAATCAAGATCCGACAGACCTTGTCTCATCAAGTTGAAT 3273  
 QY 3139 ATAAAGCCCACTTGAATACATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 3198  
 Db 3274 ATAAAGCCCACTTGAATACATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGAT 3333  
 QY 3199 ACTGGGACAGATTAACCTTGGCTTGGCTTCAATCAAGACAAAGAAAGTAAGAAAGA 3258  
 Db 3334 ACTGGGACAGATTAACCTTGGCTTGGCTTCAATCAAGACAAAGAAAGTAAGAAAGA 3393  
 QY 3359 AGAAGTAAGAACAGGGAAGAAAGATTTATTAATTTTAAACC 3300  
 Db 3394 AGAAGTAAGAACAGGGAAGAAAGATTTATTAATTTTAAATC 3435

## RESULT 2

US-09-901-511-1  
 ; Sequence 1, Application US/09901511  
 ; Patent No. 6399312  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Abbot Laboratories  
 ; APPLICANT: Wu-Ming, Jinhun R.  
 ; APPLICANT: Wang, Jiahong  
 ; TITLE OF INVENTION: THE MYOSTATIN GENE PROMOTER AND  
 ; FILE REFERENCE: 6542, US, DI  
 ; CURRENT APPLICATION NUMBER: US/09/901,511  
 ; CURRENT FILING DATE: 2001-07-09  
 ; PRIOR APPLICATION NUMBER: US 09/329,685  
 ; PRIOR FILING DATE: 1999-06-10

; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 3435  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-901-511-1  
 Query Match 43.0%; Score 1459.2; DB 3; Length 3435;  
 Best Local Similarity 72.7%; Pred. No. 0;  
 Matches 2472; Conservative 0; Mismatches 743; Indels 187; Gaps 38;  
 1 TGCTGCTCCGAAGCCATGAGAGGTTGCAATCCCGACATGAGAGAGAAACAGCTTC 60  
 Db 119 TTCTATCTGGGGCTCGAGAGGTTGCAATCAGTCCAGTGGAGAGAAATTAACCTTA 178  
 QY 61 TTGAATTTCTTGAGTACCTTTAATTCATTCATGCTGACCTCGGA-----GATTGG 114  
 Db 179 CTTAATTTCTTGAGTACCTTTAATTCATTCATGCTGACCTCGGA-----GATTGG 238  
 QY 115 ATAGAGTCACTTCATTAATTCACAGTGTATGTTCTACCAATCACTGCAACA-TGA 173  
 Db 239 ATATGATCAATTTCTCCATTTCAATGATTAATGTTCTATTAAGTCAATGCAACACTGA 298  
 QY 174 ATAAATGATTCCTGAACCACTGCCCTAGGGAACATCAAGATTAATTCCTGACCT 233  
 Db 299 GTTAGCAAAATTTGATCAATTTGTTCCAGGGAACAGGTTAGTTGAGCTCTG--- 355  
 QY 234 CTGGTCACTTTTGTGTTAATCAATCAATTAATTAATTTTGTGATTTCTGTTT 293  
 Db 356 GTCAATCAATTTAATCAATCAATCAATCAATTAATTAATTTTGTGATTTGTTT 415  
 QY 294 AAAATATCTTAATTAATTAATTAATTAATTAATTTTCAATTTGTTGTTCAACCAACAAAG 353  
 Db 416 CAATTA-CATTAATTAATTAATTAATTAATTTTCAATTTAATCACTGAACTACAGCCA---G 470  
 QY 354 CCTATTAATCAAGAGCCCTGAATGAAGCTTAATCAATCAATCAATTTTCTATGAGA 413  
 Db 471 CAGACATTAATCAAGGCTTAATGAATGATTTATATGACACA---TGCAATTTTTCATGAG 527  
 QY 414 AAAATTTTCTTGAGTCCGACAGCTTCTTGTGTTAAATTTGTTGACAAATATACA 473  
 Db 528 AACTTTTCTTGAGTCCGACAGCTTCTTGTGTTAAATTTGTTGACAAATATACA 582  
 QY 474 TAAATGAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 533  
 Db 583 AACTTTGA---TCTTAACATTTTATGATTAATTAATTAATTAATTAATTAATTAAT 633  
 QY 534 CACTTACCTTGTGTAATCATGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 593  
 Db 634 CATTCACTTGTGTAATCATGATCAATTAATTAATTAATTAATTAATTAATTAATTAAT 693  
 QY 594 AATTGAATCTGATCATTAATGAATGATGATGATGATGATGATGATGATGATGATGAT 653  
 Db 694 GACTG-AACTGATCATTAATGAATGATGATGATGATGATGATGATGATGATGATGAT 743  
 QY 654 CAGCCCTGCGGACCAATCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 710  
 Db 744 CAGTCCCTGCGGACCAATCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGAT 803  
 QY 711 -----CAGCCTTCAACATCACTAGCTTGGGGGCACTGT-----AAGCAACGATC 756  
 Db 804 GAACACACGAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
 QY 757 ACTCCCTACGCGCACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 816  
 Db 864 AAGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 923  
 QY 817 AAAAGGCTGCTGCT--AAGTATGAGGCTGAAC--AAGCAGAGATTTGATAGT 871  
 Db 924 AAAAGGAGATTTGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 983  
 QY 872 TGACCTGAGCTGAGATCTGTTGTTGG--AAGCTCAATTTTCAATTTGTTGTTGAT 929

Db 984 TGACCTATCTGGGAACCTGTGGCGTACAGATAGAGCTCAAAATTTTGGCCGCTGTGAAT 1043  
Qy 930 AGCGAACAATGCTTATATAAAGACGTGTAGAGTGAATTAAGAAATTAATTCAG 989  
Db 1044 GCCAGCGAATACGAAAAA---TGCTAGGAATATGAGTTTCATTAATTAATTTAGC 1099  
Qy 990 CAAGACATTAATGTGCAGACAGGGATCCATGAATTAAGAGCACTGACAT--GTGAAA 1047  
Db 1100 AAGTAGCAAAATTTGTGAAATACAGAAATCATGAATTAAGAAATTTGTCTGTAGCGAAA 1159  
Qy 1048 TGATTAATCTTTGTTCTTTATTCAGGACAGTAAGAGAAAGCG------T 1093  
Db 1160 TGACAACTTTGTTCACTTTTTCAGAGGTGAATGAATTAAGAGCTGGAACATGCTGT 1219  
Qy 1094 CACAGGCTGCTTACACCAATTTTCTAGAGAGCTAGCTATGTACAGCG------ 1144  
Db 1220 AACCTGGCTGCTTAGAAATTTTACTTGCTCAAGGCTTAGAAAGTGAAGCTTTGTAGC 1279  
Qy 1145 ---TAGCTGGCAATTACAAAGCAAGTCTAGTTCATGTGAGAGTGAATTTAACCA 1201  
Db 1280 TGATTAATGGAGCTATAGCTGAGAGCACTTCAATGTGAGAGCAATTTTAAACA 1339  
Qy 1202 TAACTCAACCCCTCTGCTATGAAACAGAGACTAAGTACTCAAGTACAGTATCAGCA 1261  
Db 1340 TAACTCAACCCCTCTGCTATGAAACAAAGAGCAAGCACTCAATGCGCAGTTATCAATTA 1399  
Qy 1262 CTACTATATAGACAGGCACTGTACTCAACATTTTCAATGTATTTGAATTAATCAATCCCC 1321  
Db 1400 CTACTATATAGACAGGCTCCATATTCACAGCAATTTTCAAGCAATTAATTAATTAATCCCC 1459  
Qy 1322 CAACCTCTATGAGAGCTGAAGGTTAG----AAGTATCTCATTCATTTATACACA 1376  
Db 1460 CAAAACCTATAGAGAGCTAAAGTTTAGGAAAGTTAAAGTATCTCATCTCATTTATACATA 1519  
Qy 1377 GT-----GGCAACTGAGATCTGAACTCAGGTCTATCCAACTCCAGAGCTGAGATC 1428  
Db 1520 GTTAGAGGTGCAAGTTGAGATTTGAATCTGAGTCTATCTGACTCCAGAGCTGAGTTC 1579  
Qy 1429 CCAATTTGCTACCAATTTCTAATCAAGTTAAAGGAAAAAGATTTGATTTGCTCAGAG 1488  
Db 1580 TCAATTTCAACGTGCTATACAAATTTCTAGAGCATTTAAAAAAAGTTGACTTAGAAC 1639  
Qy 1489 TGTATAGGGGCAATAGTTACA---ATTATACATTACAAAGATTTATATGTTGAAAAATA 1545  
Db 1640 TGTATAGATGATGCTTATGATCATTAATTTGAAAGATTTAGCAATTTGAAAAATG 1699  
Qy 1546 AATTTATCAAACAATAAACTTTATAGCCTGATCTAATACTGCTCCGCAACAAAGACT 1605  
Db 1700 AATTTACCAAACAATAAACTTTAGAGCCAGATCTAATATTTGCCATTAACAAAGAGT 1759  
Qy 1606 ATCTGAATCTTTGAGGGGATCTGTTGTCTGTCTGTTTCTTAAATCTTTAATGATGG 1665  
Db 1760 ATCTGAATCTT---TCAGGGGATCTGTTGTGTGTTTCTTAAATCTTTAATGATGG 1818  
Qy 1666 CAATCTAATGATTAATGTAAGGCA--TTTTTCTCAAGAGATGTAATACCTTTAAGA 1724  
Db 1819 CAATCTCAATGATTAATGTAAGGCAATTTTCTCAAGAGATGTAATACCTTTAAGA 1878  
Qy 1725 AATTGATGAAAATGCAATTAATCTTTGAGGCTAAGTTGCAATTTTATGCACTGAGCA 1784  
Db 1879 AATTGATGAAAATGCAATTAATCTTTGAGGCTAAGTTGCAATTTTATGAGCAGCGGCA 1938  
Qy 1785 GTAATTAATGTAATGTAATGTCGAAA---GTAGTGAATTTAAAAATTAATTTGATATGA 1841  
Db 1939 GTAATTAATGTAATGTAATGTCGAAAATGTAATGTAATTTAAAAATTAATTTGATATGA 1998  
Qy 1842 ACCAGTGAATCTCTGTTG--GGAATAAAGTAATGATTAATCTCTTAGAGAGTCTTAGCT 1900  
Db 1999 GCACTGTAATCTCTTTGAAAAAAAGTAATGATTAATCTCTTAGAGAGTCTTAGCT 2058  
Qy 1901 TCCCAAAAGTAATGAAAAATTAATCTCTGTGGCTGGAACAGCTTCTGTCTTG 1960

Db 2059 TCCCAAAAGAGTAGAAAAAGAAATCTCTTGGCCTAGAAATATCTTCTGTTCTTG 2118  
Qy 1961 CTGAGCTATATTTGTTAGTTTAAATAGTTCAATTTGATTAAGACCTGTGGCTCCCAAG 2020  
Db 2119 CTGAGCTATGTTGTTAGCTCTTTAATAGTTCAATTTGATTAAGATCTGTGGCTCCCAAG 2178  
Qy 2021 CTAAAGTTGAGAGTTGATCTCTTACAGAGGCACTTCAATTTAGAGAAACAAAGGCCCA 2080  
Db 2179 CTAAAGTTGAAACGTTGATCTCTACAGAGGCACTTCAATTTAGAGAAACAAAGGCCCA 2238  
Qy 2081 TTTCTGCTCCCAAGACCTTACCCCAATCCCTGCAAGTGTGCGCTCCGCTCAAAATGA 2140  
Db 2239 TTTCTGCTCCCAAGACCTTACCCCAATCCCTGCAAGTGTGCGCTCCGCTCAAAATGA 2298  
Qy 2141 GAACTGCAAAAGAAATGACTAGAGAGTGCACAGTACTAGAAATGAAAAATGACTA 2200  
Db 2299 AGAATTTGGCAAGGGTGCAGAA------TA 2325  
Qy 2201 GCACACTAAGAGAGAGAAAGAAATGAGGACCTTCAATGATGTGTTCTTCCCTTCT 2260  
Db 2236 TCGAGTATTTGGAAACAAAGAGTCAACCTTTATCATGATGCTCTTCTTAT 2385  
Qy 2261 GTGTTCAATGCTCCGATATTAATTTACAGAGGTAGATA-----ACTACATTTT 2312  
Db 2386 GTGCTCATTAATTTCTGATTAATTTTAGAAATGATGCACTTTTACTCTCTGG 2445  
Qy 2313 TCTTTACACTGGAAGCTGAGAAAACTTGTATCCATCATTAATTCATATCTTC 2372  
Db 2446 ATATTACTGCTGAAATCTGAGCAATCTGTATATCTGCGAGCCAGTTATATAA 2505  
Qy 2373 TAACTATCTATGTTATTTCTAGA-----TCAATAGCTGACAAATCTCTTTGTA 2426  
Db 2506 TTCAATTAATTAAGTATGTTCAAGAGATTTTCTACAGCTGAGGATTAACCTCTTGTA 2565  
Qy 2427 TAAACATGAAAAACATCTCTGAGCAATTAATCTGCAACTTTAGATGGAAGT 2486  
Db 2566 TAAACATG--AAAAACATCTCTGAGTATGTTAATCTGCACTTTAGATGGAAG-- 2622  
Qy 2487 AACTTAATCTAGTCAATTTGAACTGAATCAATTTTCAATGATTAATGAATAT-- 2542  
Db 2623 ---ATAATAGCACTGACAAAGTTCAGTATTAATTTTCAATTAATTAAGACATGAA 2679  
Qy 2543 -TATTTAAAGTAAATTCATGAGCAATTAATTA--AAGTAGATTTCTATGTGT 2600  
Db 2680 CTATGTAATAATTAATTCATGACAAATGTTAATTAATTAATTAATTAATTAATTAAT 2739  
Qy 2601 AAGAAATTAATCAGGAAACAGTTTCTCAATTAATGAGAGAAATCTTTAAGTATC 2660  
Db 2740 AAGAAATTAATC--GAAACAGATTTCTCAATTAATGATTAATTAATTAATTAATTAAT 2798  
Qy 2661 ACAGCTTTGATTTAAGTC--TTCCTGAATAATCTGATTTTCTAATTAATCAAGACTA 2729  
Db 2799 ATATCTTAATCTTTAATTAAGCTCTTCTAATTTTATTTTCTAATTAATCTGACACTA 2858  
Qy 2720 AAAATTAATTAATTAATTAATTAATTTT--TACTTCAATGCTTAAATAGTA 2778  
Db 2859 AAAATTAATTAATTAATTAATTAATTTTCTACTTCAAAATCTGCTTAAACAAATA 2918  
Qy 2779 TAAATCAATTTTATTTTCTGAGGAAAGCAATCACTTTTAAATGTAAGTAAAT 2838  
Db 2919 TAAATCAATTTTATTTTGGAGAAATATTTTC--ATATTTTAATTAATGTAATTAAT 2977  
Qy 2839 TAAATTAATCACTTAATTAATTAATTTTAAAGTTTCAATTAATTAATTAATTAAT 2898  
Db 2978 TAAATTAATCACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3037  
Qy 2899 TAAATTAATTAATTAATTAATTAATTAATTTTATTTTCCATGCTCAATTAAT 2958  
Db 3038 ---AGTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3093  
Qy 2959 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3018  
Db 3094 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3153

QY 3019 TAACAAAATCTGTTGGTGACTTGTGACAGACAGGGTTTAACTCTGACAGCAGATT 3078  
Db 3154 TAAACAATACTGCTGTGGTGACTTGGACAGACAGGTTTAACTCTGACAGCAGATT 3213  
QY 3079 CATTGTGAGCAGACGCCAATCAAGATCCGACAGACACTGTCTCATCAAAAGTTGGAAT 3138  
Db 3214 CATTGTGAGCAGACGCCAATCAAGATCCGACAGACACTGTCTCATCAAAAGTTGGAAT 3273  
QY 3139 ATAAAGCCCACTTGGAAATACGATTAAGATTCACGTGTGTGGCAAGTTGTCTCTAG 3198  
Db 3274 ATAAAGCCCACTTGGAAATACGATTAAGATTCACGTGTGTGGCAAGTTGTCTCTAG 3333  
QY 3199 ACTGGCAGGCAATTACGCTTGGCTTGGCGTTACTCAAAAGCAAAAGAAAGTAAAGGA 3258  
Db 3334 ACTGACATGATTAATTTTGGCTTGGCATTACTCAAAAGCAAAAGAAAGTAAAGGA 3393  
QY 3259 AGAAGTAAAGCAAGGAAAGATTTGATTTTAAACC 3300  
Db 3394 AGAAGTAAAGCAAGGAAAGATTTGATTTTAAATC 3435

## RESULT 3

US-09-626-959D-1  
; Sequence 1, Application US/09626959D  
; Patent No. 6617440  
; GENERAL INFORMATION:  
; APPLICANT: Findlay, Robert  
; TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AND  
; TITLE OF INVENTION: METHODS FOR ITS USE  
; FILE REFERENCE: PCI0448A  
; CURRENT APPLICATION NUMBER: US/09/626,959D  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,540  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2482  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-626-959D-1

Query Match 15.5%; Score 525; DB 4; Length 2482;  
Best Local Similarity 61.5%; Pred. No. 1.2e-112;  
Matches 1256; Conservative 0; Mismatches 665; Indels 122; Gaps 21;

QY 1188 GATGAATTTAAACATATCTCAACCCCTCTGCATGAAACAGAGACTAAGTACTGAAGTA 1247  
Db 521 GAAGCACTTGAGATTAATTTGAAAGTAAAGGCTTGAACAAAGAGCAAGCCCTTCTGCT 580  
QY 1248 CCAGTTATCAGTCACTTACTATATG-----ACAGCACTGTACTCAACATTTAAT 1299  
Db 581 TCAAGTATTAATTAATCTATGAAAGGAGACTACATTTAGCTACTTATATGCTAAATTAAT 640  
QY 1300 GTATTAATTAATTAATCATGCCCCCACTCTATGAGAACTGAGGTTAGAGAGTATC 1359  
Db 641 GCCTCAAAACCCCTTATGTTGAGAACTAAAGATTAAGAGTAAAGTATGCTGTCCCTCT 700  
QY 1360 TCATTCATTATTAACAGATGCGAACTGAGATCTGAATCTGAGGTATCAACTCCAGGA 1419  
Db 701 TGTATCATCTTAGAAGAGGCAAAATGAGATTGAATCTCAGGTTTATTTGACTCTTCA 760  
QY 1420 CCTGAGATCCCAATGCTACCAATTTCTAATCAAGTTAAAGGAAAGAAAGATTTGATTT 1479  
Db 761 TCTGAGCTCAACATGCGACGTACTAAGAAAGAAAGAAAGAAAGTCAAGATCA---ATT 816  
QY 1480 GCTCAGAGTATATAGGGGCAATATGTAC---AATTATACATTAACAAGATTTATATGT 1536  
Db 817 CCTGAGATTAATATAGCAGCATGTGTATGATTAATTAATGATCAAGAAAGATTTATATGC 876  
QY 1537 TGAATAATTAATTAATCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1596

Db 877 AGAAAAATGAATTTTCCAGACAAATCTGATTTATAGCCTGCTCTAATATTTCTGTGA 936  
QY 1597 ACAAAGACTATCTGAATTCCTTCAGGGCATCTGGTTGTGTGGTTTCTTAATCTTT 1656  
Db 937 --TAAAGGGGCAATCACTCAGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 994  
QY 1657 AATGATGGCAATCTAATGATTAATGTAAGGCCA-----TTTTTCTCAAGAGATGTA 1711  
Db 995 AATGATGGCAATCTAATGATTAATGTAAGGCCA-----TTTTTCTCAAGAGATGTA 1054  
QY 1712 ATACCTCTTAAGATTTGATGAATGATTAATGATTAATGATTAATGATTAATGATTA 1771  
Db 1055 ATGCTCTTAAGATTTGATGAATGATTAATGATTAATGATTAATGATTAATGATTA 1114  
QY 1772 GTGACATGAGCAGTAATTT---AGTGTCAATGTGGGAAAGTGTGACTTAAATTA 1828  
Db 1115 GTGACATGAGCAGTAATTT---AGTGTCAATGTGGGAAAGTGTGACTTAAATTA 1174  
QY 1829 ATATTTGATTAATGAACCACTGCACTCTTGTGGGG-----AAAAAGTAAATGATTAAC 1880  
Db 1175 ATATTTGATTAATGAACCACTGCACTCTTGTGGGGGTGTGTGAAGGGGATTAATGAAT 1234  
QY 1881 TCTCTTAGAGATCTTACCTTCCCAAAAGTATGTAAGAAATTAATCTCTGTGGCTG 1940  
Db 1235 ATCTTAAGACCTCTCAGCTTCCCAAGAGAGGAGAA-----CTCTGTGGCTG 1285  
QY 1941 GAAACAGCTTCTGTTCTGTGGCTATATTTGTTAGTTTAAATGATTAATGATTAAT 2000  
Db 1286 GAAGGTCTCTGTGCTCCT--GCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1343  
QY 2001 AGACCTGTGTGCTCCCAAGGTAAGTGAAGTTTGAATCTCTCAAGAGGCACTTCAAT 2060  
Db 1344 CGATCTGTGTGCTCTTAAGGCAAGGTAAGTGAATCTCTCAAGAGGCACTTCAAT 1403  
QY 2061 TTGAAGAAACAAAGCCCAATTTCTGTCTCCCAAGCTTCAAGGCAATCTCTGTGAGTG 2120  
Db 1404 TCAGAGAAACAAAGCCCAATTTCTGTCTCCCAAGCTTCAAGGCAATCTCTGTGAGTG 1462  
QY 2121 TCTGCTCTGTGCTCAAAATGAGAGAGGCTGCAAGGAGTGTGAGAGTGTGAGAGTGT 2180  
Db 1463 TCTGCTCTGTGCTCAAAATGAGAGAGGCTGCAAGGAGTGTGAGAGTGTGAGAGTGT 1518  
QY 2181 GAAAGTAAAGAAATGAGACTGACACATCTGAGAGAGCAAGAAATGAGGCACTTCAATGA 2240  
Db 1519 -----GGAGAGCAACAAAGAGCAACCCCTCTTACA 1547  
QY 2241 TGTGTCTCTTCCCTTCTGTGTGTTCAATATCTCGATTAATTTACAGAGGTAGATA 2300  
Db 1548 ---TGCACTTGTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1603  
QY 2301 ACTACATTTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2351  
Db 1604 ---TTGCACTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1660  
QY 2352 ATCAATTAATTAATCAATCTTAACTGATTTTGAATTTTGAATTAATTAATTAATTAAT 2411  
Db 1661 TACTTCAAAATTAATCAATCTTAACTGATTTTGAATTTTGAATTAATTAATTAATTAAT 1720  
QY 2412 ATATCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2471  
Db 1721 GGAATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1780  
QY 2472 TTTAGATAGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2531  
Db 1781 ATCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1840  
QY 2532 ATAAAGATTAATTT---TTAAAGTATTTCTAGAGCAATTTATTAATTAATTAATTAAT 2586  
Db 1841 GTCAAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1900  
QY 2587 TTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2646  
Db 1901 TTTGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1960

QY 2647 CTTTACTAGTACAGCTCTTTTCATTAGTCTCTGTAATAATCTGATTTTCTAA 2706  
DB 1961 TTTTAGCAGGGTCAAACTCAGCTTCTTTAAATTAAGTACGCTCTTCAGTTTAC 2020  
QY 2707 TTATACAGACTAAATAATTTATATTAACAAATAAATTTTATTTTAACTTCAATGCTT 2766  
DB 2021 TTCT-----CTAATTAACGACCTTAACGCAATTTTTCCTCAATATTA 2068  
QY 2767 ACTTAATAGTATAAATCATTTTATTTTCTGAGGAAAGCAATCACTTTTAACTA 2826  
DB 2069 GTTTTATTAACAAACAGCCTCCAGCTCAAGATTAACATTTCTA-TTTTAAACA 2127  
QY 2827 TGAAGTAAATTAAGTATTTTATCAATTAATTTTAAAGTTTCAATTAAG 2886  
DB 2128 CAAATCTAAATTAATAATTAATTAATTAATTAATTTTAAAGTTTCAATTAAG 2180  
QY 2887 ATGAATTAAGTCTAAGTATATGTTATTTTAAATTAAGTTTAAATTTTTCGATGCA 2946  
DB 2181 ATTATTAAGCTTTAAGTACAGTTTATATTAAGT-ACAGAGCTTCAATTTTCAATGCA 2239  
QY 2947 CATACAGCTTTATTTATTTATTTATTTTCTTTTAAAGTATCAATGATCAGCT 3006  
DB 2240 CATATATCTTTCAATTTGAGGATTTATTTTCAATTTATGAAGTCAATGAATCAGCT 2239  
QY 3007 CACCTTGAAGTAAACAAATATCTGTTGAGTCTTGAAGAGAGGTTTAACTCT 3066  
DB 2200 TGCCCTCAGCTGAACAAATGCTGCTTGAGCTTGAAGAGAGGTTTAACTCT 2359  
QY 3067 GACAGCGAGTTCATTTGAGCAGAGCCCAATCAAGATCCGAGCACTTGTCTCAT 3126  
DB 2360 GACAGCGAGTTCATTTGAGCAGAGCCCAATCAAGATCCGAGCACTTGTCTCAT 2419  
QY 3127 CAAAGTGAATTAATAAGCCACTTGAATACAGTATTAAGATTTCACTGTGTGCA 3186  
DB 2420 CTAAGTTGAATTAATAAGCCACTTGAATACAGTATTAAGATTTCACTGTGTGCA 2479  
QY 3187 GTT 3189  
DB 2480 GTT 2482

RESULT 4  
US-09-626-959D-2  
; Sequence 2, Application US/09626959D  
; Patent No. 6617440  
; GENERAL INFORMATION:  
; APPLICANT: Findlay, Robert  
; TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AN  
; FILE REFERENCE: PCI0448A  
; CURRENT APPLICATION NUMBER: US/09/626,959D  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,540  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 2  
; LENGTH: 1537  
; TYPE: DNA  
; ORGANISM: Sus scrofa  
US-09-626-959D-2

Query Match 14.6%; Score 494.8; DB 4; Length 1537;  
Best Local Similarity 83.7%; Pred. No. 1.2e-105;  
Matches 676; Conservative 0; Mismatches 102; Indels 30; Gaps 9;

QY 2395 AGATCAATATGCTGCAATATCTCTTTGTATTAACATGAAACAAACATCTCTGAG 2454  
DB 747 AATATATGAACTGACATTAATCTCTGTTGATTAACATGAAACAAACATCTCTGAG 806  
QY 2455 CAATATTAATCTGCACTTTAGATAGAAAGTAACTTAATACATGCAATGAACTGAA 2514

DB 807 CAATATTAATCTGCACTTTAGATAGAAAGTAACTTAATACATGCAATGCA 855  
QY 2515 ATCAATTTTCAATGATTAATAAGATATTTTAAAGTATTCATGAGCAATTTAATA 2574  
DB 856 GCAGATTTTCAAGTGAATTAAGATATTTTAAAGTATTCATGAGCAATTTAATA 915  
QY 2575 TTA-AAGTAGATTTTCAATGATTTTAAAGATTTTCAAGGAAACAGTTTCTCAAT 2633  
DB 916 GAATTAAGTATGATTTTCAATGATTTTAAAGATTTTCAAGGAAACAGTTTCTCAAT 975  
QY 2634 TATAGCAAAATTTTCAATGATTTTAAAGATTTTCAAGGAAACAGTTTCTCAAT 2687  
DB 976 TATAGCAAAATTTTCAATGATTTTAAAGATTTTCAAGGAAACAGTTTCTCAAT 1035  
QY 2688 ATAAATCTGATTTT-TCATATTAACAGACTAAATAATTTTAAATTAACAAATAAAT 2746  
DB 1036 TTAATCTGATTTTCTGATTTTCAAGGAAACAGTTTAAATAATTTTAAACAGAAATTAAT 1095  
QY 2747 TATTTTAACTTCAATGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 2806  
DB 1096 TCTTTTCTCAATGATTTTCTGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 1155  
QY 2807 --GATATCACTTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 2864  
DB 1156 AGACATTTTCACTTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 1211  
QY 2865 TTTTAAAGTTTCACTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 2921  
DB 1212 TTTTAAAGTTTCACTTAAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 1271  
QY 2922 AAAGTTTAAATTTTTCGATGTCATACATGAGCTTTTATTTATTTATTTTCTTT 2981  
DB 1272 ATAGATTTTAAATTTTTCGATGTCATACATGAGCTTTTATTTATTTATTTTCTTT 1331  
QY 2982 TAAAGATTTTAAATTTTTCGATGTCATACATGAGCTTTTATTTATTTATTTTCTTT 3041  
DB 1332 TATGAAGTATTAATAAGATTTTAAAGATTTTAAAGATTTTAAAGATTTTAAAG 1391  
QY 3042 TGTGACAGACAGGTTTAACTCTGACAGAGGATTTTAAAGATTTTAAAGATTTTAAAG 3101  
DB 1392 TGTGACAGACAGGTTTAACTCTGACAGAGGATTTTAAAGATTTTAAAGATTTTAAAG 1451  
QY 3102 CAGATCCGACAGACCTTTCTCATCAAAAGTTGCAATTTAAAGCCACTTGAATACAG 3161  
DB 1452 TAGATCTGACAGACCTTTCTCATCAAAAGTTGCAATTTAAAGCCACTTGAATACAG 1509  
QY 3162 TATTAAGATTTCACTGTTGAGGCAAGTT 3189  
DB 1510 TATTAAGATTTCACTGTTGAGGCAAGTT 1537

RESULT 5  
US-09-354-409-1  
; Sequence 1, Application US/09354409  
; Patent No. 6555672  
; GENERAL INFORMATION:  
; APPLICANT: Li-fang Liang  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR PROMOTER AND USES  
; FILE REFERENCE: MTN-027  
; CURRENT APPLICATION NUMBER: US/09/354,409  
; CURRENT FILING DATE: 1999-07-15  
; EARLIER APPLICATION NUMBER: 60/092,865  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: 60/123,270  
; EARLIER FILING DATE: 1999-03-08  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO: 1  
; LENGTH: 649  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-354-409-1

Query Match 12.5%; Score 422.4; DB 4; Length 649;  
Best Local Similarity 82.0%; Pred. No. 6,6e-89;  
Matches 536; Conservative 0; Mismatches 111; Indels 7; Gaps 4;

```
QY 2652 ACTACTATCAGAGCTTTTTCATTAAAGTC-TTCCTGAATTAATCTGTATTTCTAATAT 2710
DB 1 ACTAGTATCATATATCTTAACTTTTAACTCAGGCTCTTCAATTTTATTTTCTTAATAC 60
QY 2711 ACAAGACTAAATATTAATATATAACAATATAATATTTT-TACTTCAATAGCTTACT 2769
DB 61 TTGGCACTTAATAATATTTAATACAAATATAATATTTTCTACTTCAATATCTTGC 120
QY 2770 TAAATATTAATAATCAATTTTATTTTCTGAGGAAAGCATATCACTTTTAACTATGA 2829
DB 121 TAAACAAATATAAATCATTTTATTTTGAAGAAATATTTTC-ATATTTAAATATGT 179
QY 2830 AGCTAAATTAAGATTTATCTTAATATTAATTTTAAAGTTTCATATTAAGATG 2889
DB 180 AGTATAAATTAATAATGCTTATTTTAAATTAACAATAGAGTGTGTGAGATTAAGTA 239
QY 2890 AATAAGATCTAAGTATATGTTATTTGTTAATAAGTTTAAATTTTTCGATGTCACAT 2949
DB 240 TTTAAG---TACGTTTATATTTTCCACATGACTTTGTTTTCAAATGTCACAA 295
QY 2950 ACAGCCTTTATTTATCATAGATTTATTCCTTTTAAAGATGATCAATGATCACTGAC 3009
DB 296 ATATCTTTTATTTATTTAGATTTATTTCTTTATGAAGTACAAATGATCACTGAC 355
QY 3010 CCTTACCTGTAACAAATATCTGTTTGCTGATCTTGACAGACAGGTTTAACTCTGAC 3069
DB 356 CCTTACCTGTAACAAATATCTGTTTGCTGATCTTGACAGACAGGTTTAACTCTGAC 415
QY 3070 AGCGAGATTCATGTCGAGCAAGACCAATCAAGATCCGACGACCTGTCATCA 3129
DB 416 AGCGAGATTCATGTCGAGCAAGACCAATCAAGATCCGACGACCTGTCATCA 475
QY 3130 AGTTGAATATTAATAAGCACTTGGATTAAGATTAAGATTAAGATTAAGATTAAGAT 3189
DB 476 AGTTGAATATTAATAAGCACTTGGATTAAGATTAAGATTAAGATTAAGATTAAGAT 535
QY 3190 GTCTCTGAGCTGGGAGGACATTAAGTTGGCTTGGGCTTCTCAAAAAGCAAAA 3249
DB 536 GTCTCTGAGCTGGGAGGACATTAAGTTGGCTTGGGCTTCTCAAAAAGCAAAA 595
QY 3250 GTAAAAAGAAAGTAAGAAACAAGGAAAGATGTGATTTGATTTAAACCATG 3303
DB 596 GTAAAAAGAAAGTAAGAAACAAGGAAAGATTTATTTGATTTAAATCATG 649
```

RESULT 6  
US-09-626-959D-2/c  
; Sequence 2, Application US/09626959D  
; Patent No. 6617440

; GENERAL INFORMATION:  
; APPLICANT: Findlay, Robert  
; TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AN  
; TITLE OF INVENTION: METHODS FOR ITS USE  
; FILE REFERENCE: PCI0448A  
; CURRENT APPLICATION NUMBER: US/09/626,959D  
; CURRENT FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,540  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 1537  
; TYPE: DNA  
; ORGANISM: Sus scrofa

US-09-626-959D-2

Query Match 9.8%; Score 332.8; DB 4; Length 1537;  
Best Local Similarity 63.9%; Pred. No. 7.8e-68;

Matches 555; Conservative 0; Mismatches 302; Indels 11; Gaps 3;

```
QY 2485 GTAACCTAATCTAGTCAATTTGAACAAATATACATTTTCATATGAATATAAAGATATTA 2544
DB 1223 GAACCTTTAAATTTGTAATTTAAATAGTAATCTTTTACACTCATCTTAAAGATTG 1164
QY 2545 TTTAAAGTAATTCAGTACAGCAATTAATTAATTAAGATGATTTTCATTATGTGTAAGA 2604
DB 1163 AAATGCTTTTCCCAAAAAAATAAATGATTTTACATTTATTTAGACAAACATTTGAGG 1104
QY 2605 ATTTATGAGGAAACAAGTTTCTCAATTTATAGAGAAAATCTTTACTGTATACAG 2664
DB 1103 AAAAAAGATTTTATTTGCTGTTTAAATTTATTTTACCTGCTGTATTCAGAGAAATAC 1044
QY 2665 TCTTTCAATTAAGCTTCTGTAATTAATCTGATTTTCTAATTTATACAGCTAAAT 2724
DB 1043 AGATTTAAATTTGGAAGACCTGAATTA---ATTTAAGATTTGATACATGTAATTA 988
QY 2725 AATTTAATATAACAATTAATTAATTTTACTTCAATGCTTACTTAATATGATATAAT 2784
DB 987 TATTACGCTAATATTGAGAACTGTTTCTGACTAAATTTCTAGTACATTAATGAGAAA 928
QY 2785 CATTTATTTTCTGAGGAAAGCATATCACTTTTAAATGATGAAAGTAAATTAAGAT 2844
DB 927 TCATACCTTAATCTGTTATTAATTAACATGAAATTTTAAATTAATCTTTTATTCAG 868
QY 2845 TTATTCATTAATTAATTAATTTTAAAGTTTCAATATAAAGATGAATGAATCAAGT 2904
DB 867 TGAATATGCTGCTCACTTTTCACTGATTTTCTCTATTCCTTAAGTTGCAATTAATTA 808
QY 2905 TATATGTTATTTTAATTAAGTTTAAATTTTTCGATGTCATATCAAGCTTTATTAAT 2964
DB 807 GCTCAGAGATGTTGTTTTCATTTGTTATTAACAAGAGTAATGTCAGTTTATTAAT 748
QY 2965 CATGATTTATTTCTTTTAAAGATGATCAATGATAGTCACTCACTTGTACTGTAACA 3024
DB 747 TGTGATTTATTTCTTTTAAAGATGAATGAATGATGATCACTTGTACTGTAACA 688
QY 3025 AATACCTGTTGGTGACTTGTGACAGACAGGTTTAACTCTGACAGGAGATTCATTT 3084
DB 687 AATACCTGTTGGTGACTTGTGACAGACAGGTTTAACTCTGACAGGAGATTCATTT 628
QY 3085 GGAGCAAGGCAATCAAGATCCGACGACACTTGTCTATCAAAAGTTGGAATTAATA 3144
DB 627 GGAGCAAGGCAATCAAGATCCGACGACACTTGTCTATCAAAAGTTGGAATTAATA 570
QY 3145 AGCACTTGAATACATATTAAGATTAAGATTAAGTGTGTGCAAGTGTCTCAAGCTGG 3204
DB 569 AGCACTTGAATACATATTAAGATTAAGTGTGTGCAAGTGTCTCTCAGACAGTG 510
QY 3205 CAGGATTAAGCTTTGCTGCGCTTACTCAAAAGCAAAAAGTAAGTAAGTAAGTAAGT 3264
DB 509 CAGGATTAAGCTTTGCTGCGCTTACTCAAAAGC-----AAAGTAAGTAAGTAAGT 455
QY 3265 AAGAAACAAGGAAAGATTTGATTTTAAACATGCAAAAACCTGCAATCTCTGT 3324
DB 454 AAGAAACAAGGAAAGATTTGATTTTAAACATGCAAAAACCTGCAATCTCTGT 395
QY 3325 TATATTTACTTATTTATGCTGATTTG 3352
DB 394 TATATTTACTTATTTATGCTGCTATCTG 367
```

RESULT 7  
US-09-354-409-4  
; Sequence 4, Application US/09354409  
; Patent No. 6555672

; GENERAL INFORMATION:  
; APPLICANT: Li-fang Liang  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR PROMOTER AND USES  
; TITLE OF INVENTION: THEREFOR  
; FILE REFERENCE: MTN-027  
; CURRENT APPLICATION NUMBER: US/09/354,409



LENGTH: 158  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-354-409-7

Query Match 4.2% Score 143.6; DB 4; Length 158;  
Best Local Similarity 94.3%; Pred. No. 4.7e-24;  
Matches 149; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2985 GAAGTAGCAATGATGAGCTGACCTGACCTGTAACAAATATGTTGGTGAATCTGT 3044  
DB 1 GAAGTAGCAATGATGAGCTGACCTGACCTGTAACAAATATGTTGGTGAATCTGT 60  
QY 3045 GACAGACAGGGTTTAACTCTGACAGGAGATTCATTGTGAGCAGCAATCAG 3104  
DB 61 GACAGACAGGGTTTAACTCTGACAGGAGATTCATTGTGAGCAGCAATCAG 120  
QY 3105 ATCCGACGACACTTGTCTCATCAAGTTGCAATTTAA 3142  
DB 121 ATCTGACGACACTTGTCTCTTAAGTTGCAATTTAA 158

RESULT 11  
US-09-354-409-8  
Sequence 8, Application US/09354409  
Patent No. 6555672  
GENERAL INFORMATION:  
APPLICANT: Li-Fang Liang  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR PROMOTER AND USES  
TITLE OF INVENTION: THEREFOR  
FILE REFERENCE: MTN-027  
CURRENT APPLICATION NUMBER: US/09/354,409  
CURRENT FILING DATE: 1999-07-15  
EARLIER APPLICATION NUMBER: 60/092,865  
EARLIER FILING DATE: 1998-07-15  
EARLIER APPLICATION NUMBER: 60/123,270  
EARLIER FILING DATE: 1999-03-08  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8  
LENGTH: 156  
TYPE: DNA  
ORGANISM: Sus scrofa  
US-09-354-409-8

Query Match 4.2% Score 141.8; DB 4; Length 156;  
Best Local Similarity 98.6%; Pred. No. 1.2e-23;  
Matches 143; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2985 GAAGTAGCAATGATGAGCTGACCTGACCTGTAACAAATATGTTGGTGAATCTGT 3044  
DB 1 GAAGTAGCAATGATGAGCTGACCTGACCTGTAACAAATATGTTGGTGAATCTGT 60  
QY 3045 GACAGACAGGGTTTAACTCTGACAGGAGATTCATTGTGAGCAGCAATCAG 3104  
DB 61 GACAGACAGGGTTTAACTCTGACAGGAGATTCATTGTGAGCAGCAATCAG 120  
QY 3105 ATCCGACGACACTTGTCTCATCAAGTTGCAATTTAA 3129  
DB 121 ATCTGACGACACTTGTCTCTTAAGTTGCAATTTAA 145

RESULT 12  
US-08-891-789B-1  
Sequence 1, Application US/08891789B  
Patent No. 6103466  
GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel  
TITLE OF INVENTION: Double-Muscling in Mammals  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West

CITY: Toronto  
STATE: Ontario  
ZIP: M5L 1A9  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,789B  
FILING DATE: July 14, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 52836/00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344  
TELEFAX: (416) 863-2653  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1196 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-891-789B-1

Query Match 4.0% Score 134.4; DB 3; Length 1196;  
Best Local Similarity 99.3%; Pred. No. 1.5e-21;  
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3255 AGAAGAAGTAAGAACAAGGAAGATTTGATTGATTTTAAACATGCAAAACTGCA 3314  
DB 1 AGAAGAAGTAAGAACAAGGAAGATTTGATTGATTTTAAACATGCAAAACTGCA 60  
QY 3315 AATCTGTTTAAATTTAACTTATTATGCTGATTTGTTGCCCACTGATCTGAATGA 3374  
DB 61 AATCTGTTTAAATTTAACTTATTATGCTGATTTGTTGCCCACTGATCTGAATGA 120  
QY 3375 GAACAGGACAGAGAG 3390  
DB 121 GAACAGGACAGAGAG 136

RESULT 13  
US-08-891-789B-3  
Sequence 3, Application US/08891789B  
Patent No. 6103466  
GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel  
TITLE OF INVENTION: Double-Muscling in Mammals  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Blake, Cassels & Graydon  
STREET: Box 25, Commerce Court West  
CITY: Toronto  
STATE: Ontario  
ZIP: M5L 1A9  
COUNTRY: Canada  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3 1/2 inch, 1.4 Mb storage  
COMPUTER: COMPAQ, IBM PC compatible  
OPERATING SYSTEM: MS-DOS 5.1  
SOFTWARE: WORD PERFECT  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/891,789B  
FILING DATE: July 14, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Hunt, John C.  
REGISTRATION NUMBER: 36,424  
REFERENCE/DOCKET NUMBER: 52836/00004  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 863-4344



TELEFAX: (416) 863-2653  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1240 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-891-789B-3

Query Match 3.9%; Score 132.8; DB 3; Length 1240;  
Best Local Similarity 98.5%; Pred. No. 3.6e-21;  
Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3255 AGAAGAAGTAAGAACAGGAAAGAAAGTATGATTTTAAACATGCAAAAACGCA 3314  
DB 1 AGGAAAAAGTAAGAACAGGAAAGGAAAGTATGATTTTAAACATGCAAAAACGCA 60  
QY 3315 AATCTGTTTATATTTACTATTATGCTGATTTGCTGGCCAGTGAATGA 3374  
DB 61 AATCTGTTTATATTTACTATTATGCTGATTTGCTGGCCAGTGAATGA 120  
QY 3375 GAACAGCGAGCAGAG 3390  
DB 121 GAACAGCGAGCAGAG 136

RESULT 14  
US-09-573-080A-233  
; Sequence 233; Application US/09573080A  
; Patent No. 6828097  
; GENERAL INFORMATION:  
; APPLICANT: JOAN, KNOUL  
; APPLICANT: ROGAN, PETER  
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATI  
; FILE REFERENCE: 30307  
; CURRENT APPLICATION NUMBER: US/09/573,080A  
; CURRENT FILING DATE: 2000-05-16  
; NUMBER OF SEQ ID NOS: 479  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 233  
; LENGTH: 653  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: repeat\_region  
; LOCATION: (1)..(653)  
; OTHER INFORMATION: mer82  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: n is a, c, g or t  
; PUBLICATION INFORMATION:  
; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A  
; TITLE: Prototypic sequences for human repetitive DNA  
; JOURNAL: Journal of Molecular Evolution  
; VOLUME: 35  
; ISSUE: 4  
; PAGES: 286-291  
; DATE: 1992-10-  
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)  
; DATABASE ENTRY DATE: 1996-01-26  
; DATABASE ENTRY DATE: 1996-01-26  
US-09-573-080A-233

Query Match 3.7%; Score 126.2; DB 4; Length 653;  
Best Local Similarity 70.9%; Pred. No. 9.7e-20;  
Matches 222; Conservative 1; Mismatches 81; Indels 9; Gaps 4;

QY 119 AGCTACTCTCATTTATTCACAGGTATGTTCTACCCATACATGCCAACA-TGAATA 177  
DB 2 AGTTATCTCTCATTTATTCACAGGTATGTTCTATAAAGTACCGCAGCACTGAATA 61  
QY 178 GTGATTCCTGAACCACTGCCCTAGGGGAATCAAGATTAGTTCCTCAGCCTCTGG 237

DB 62 GCCAATACAGAACCATCGCTCTAGAGAAATACAGATTAGGTTCTCGACCTCTGG 121  
QY 238 TC---ACGTTTGTATACCATCAATTAATACTGTTGTGTCATTTCTGTTTA 294  
DB 122 TCACACATTTTATCATCAACCGATCAATATATTAACCTTTTATGTTGTGTTTA 181  
QY 295 AAATATCTTATTTAATACGTAAGTCTGTAATTTCTTCAACATTTGTTTCAACAAAGGC 354  
DB 182 AGACNNC-TTATTTAATATATATGTTGATTTTAACTGAACCTCACAGCCAAAG-- 238  
QY 355 CCAATTTACTGGAAGCCCTGAATGAAGCTTACATTAACACACATTTGTTTCTATGAGAA 414  
DB 239 -CACTATACTCAATGCTGAATGAAGCTTATCTTAACACACATTTTCTCATAAAGTA 256  
QY 415 AAATTTTCCTTC 427  
DB 297 CATCAGACCTTC 309

RESULT 15  
US-08-525-596B-13  
; Sequence 13; Application US/08525596B  
; Patent No. 5827733  
; GENERAL INFORMATION:  
; APPLICANT: Huynh, Thanh  
; APPLICANT: Lee, Se-Jin  
; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fish & Richardson P.C.  
; STREET: 4225 Executive Square, Suite 1400  
; CITY: La Jolla  
; STATE: CA  
; COUNTRY: US  
; ZIP: 92037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows95  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/525,596B  
; FILING DATE: 19-SEP-1995  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07762  
; FILING DATE: 08-JUL-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wetherell, Jr., Ph.D, John R.  
; REGISTRATION NUMBER: 31,678  
; REFERENCE/DOCKET NUMBER: 07265/075001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 619-678-5070  
; TELEFAX: 619-678-5099  
; INFORMATION FOR SEQ ID NO: 13:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2743 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; MOLECULE TYPE: Genomic DNA  
; IMMEDIATE SOURCE:  
; CLONE: Human GDF-8  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 59...1183  
US-08-525-596B-13

Query Match 3.7%; Score 126.2; DB 1; Length 2743;  
Best Local Similarity 91.2%; Pred. No. 1.7e-19;  
Matches 134; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 3243 AAGAAAGTAAGAAAGAAAGTAAGAACAGGAAAGATTTGATTTTAAACAT 3302

Db 1 AAGAAAATTAAAGAGAGAAACAGAGACAGAAAAAAGTTATATATGATTTTAAATAT 60

Qy 3303 GCAAAAATCGCAATCTCTGTTATATTTAACTATTTATGCTGATGTGGCCAGT 3362

Db 61 GCAAAAATCGCAACTCTGTTATATTTAACTGTTATGCTGATGTGGCTCAGT 120

Qy 3363 GGATCTGAATGAGAACAGCGAGCGAA 3389

Db 121 GGATCTGAATGAGAACAGCGAGCGAAA 147

Search completed: March 31, 2005, 14:45:28  
Job time : 421 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 12:46:17 ; Search time 1218 Seconds  
(without alignments)  
16845.606 Million cell updates/sec

Title: US-09-743-312D-1\_COPY\_7103\_10492  
Perfect score: 3390  
Sequence: 1 tgcgtccgcagcagcatagc.....atcgagacagcgcagcagaag 3390

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues  
Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCR\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubpna/PCITS\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10F\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match Length | DB ID                       | Description            |
|------------|--------|--------------------|-----------------------------|------------------------|
| 1          | 1459.2 | 43.0               | 3435 9 US-09-901-511-1      | Sequence 1, Appl1      |
| 2          | 525    | 15.5               | 2482 17 US-10-610-473-1     | Sequence 1, Appl1      |
| 3          | 508.6  | 15.0               | 5790 15 US-10-251-115-54    | Sequence 54, Appl1     |
| 4          | 494.8  | 14.6               | 1537 17 US-10-610-473-2     | Sequence 2, Appl1      |
| 5          | 332.8  | 9.8                | 1537 17 US-10-610-473-2     | Sequence 2, Appl1      |
| 6          | 224.8  | 6.6                | 942 13 US-10-027-632-120231 | Sequence 120231, Appl1 |
| 7          | 224.8  | 6.6                | 942 13 US-10-027-632-120231 | Sequence 120231, Appl1 |
| 8          | 190    | 5.6                | 2823 17 US-10-366-345-27    | Sequence 27, Appl1     |
| 9          | 174.4  | 5.1                | 200 17 US-10-610-473-3      | Sequence 3, Appl1      |
| 10         | 134.4  | 4.0                | 1196 15 US-10-251-115-1     | Sequence 1, Appl1      |
| 11         | 132.8  | 3.9                | 1240 15 US-10-251-115-3     | Sequence 3, Appl1      |

|    |       |     |        |                         |                    |
|----|-------|-----|--------|-------------------------|--------------------|
| 12 | 126.2 | 3.7 | 653    | 10 US-09-854-867-233    | Sequence 233, App  |
| 13 | 126.2 | 3.7 | 653    | 19 US-10-786-970A-233   | Sequence 233, App  |
| 14 | 126.2 | 3.7 | 2743   | 9 US-09-859-211-13      | Sequence 13, Appl1 |
| 15 | 126.2 | 3.7 | 2743   | 9 US-09-841-730-1       | Sequence 1, Appl1  |
| 16 | 126.2 | 3.7 | 2743   | 10 US-09-872-856-13     | Sequence 13, Appl1 |
| 17 | 126.2 | 3.7 | 2743   | 14 US-10-278-803-13     | Sequence 13, Appl1 |
| 18 | 126.2 | 3.7 | 2743   | 15 US-10-335-483-13     | Sequence 13, Appl1 |
| 19 | 126.2 | 3.7 | 2743   | 17 US-10-463-973-13     | Sequence 13, Appl1 |
| 20 | 126.2 | 3.7 | 2743   | 17 US-10-456-852-3      | Sequence 3, Appl1  |
| 21 | 126.2 | 3.7 | 2743   | 18 US-10-662-438-1      | Sequence 1, Appl1  |
| 22 | 126.2 | 3.7 | 2743   | 19 US-10-663-374-1      | Sequence 1, Appl1  |
| 23 | 104.6 | 3.1 | 2676   | 9 US-09-859-894A-10     | Sequence 10, Appl1 |
| 24 | 104.6 | 3.1 | 2676   | 9 US-09-859-211-11      | Sequence 11, Appl1 |
| 25 | 104.6 | 3.1 | 2676   | 9 US-09-841-730-3       | Sequence 11, Appl1 |
| 26 | 104.6 | 3.1 | 2676   | 10 US-09-872-856-11     | Sequence 11, Appl1 |
| 27 | 104.6 | 3.1 | 2676   | 14 US-10-278-803-11     | Sequence 11, Appl1 |
| 28 | 104.6 | 3.1 | 2676   | 15 US-10-335-483-11     | Sequence 11, Appl1 |
| 29 | 104.6 | 3.1 | 2676   | 17 US-10-463-973-11     | Sequence 11, Appl1 |
| 30 | 104.6 | 3.1 | 2676   | 17 US-10-456-852-1      | Sequence 1, Appl1  |
| 31 | 104.4 | 3.1 | 330973 | 13 US-10-087-192-1498   | Sequence 1498, Ap  |
| 32 | 103   | 3.0 | 2676   | 15 US-10-251-115-5      | Sequence 5, Appl1  |
| 33 | 102.8 | 3.0 | 55005  | 18 US-10-719-993-6968   | Sequence 6968, Ap  |
| 34 | 102.8 | 3.0 | 318760 | 18 US-10-719-993-6765   | Sequence 6765, Ap  |
| 35 | 100.4 | 3.0 | 98439  | 19 US-10-741-600-17724  | Sequence 17724, A  |
| 36 | 97.4  | 2.9 | 1182   | 13 US-10-027-632-258706 | Sequence 258706,   |
| 37 | 97.4  | 2.9 | 1182   | 17 US-10-027-632-270981 | Sequence 270981,   |
| 38 | 96.6  | 2.8 | 708    | 13 US-10-027-632-270982 | Sequence 270982,   |
| 39 | 96.6  | 2.8 | 708    | 13 US-10-027-632-270981 | Sequence 270981,   |
| 40 | 96.6  | 2.8 | 708    | 17 US-10-027-632-270982 | Sequence 270982,   |
| 41 | 96.6  | 2.8 | 708    | 17 US-10-027-632-174714 | Sequence 174714,   |
| 42 | 94.8  | 2.8 | 620    | 13 US-10-027-632-174714 | Sequence 174714,   |
| 43 | 94.8  | 2.8 | 853    | 13 US-10-027-632-157095 | Sequence 157095,   |
| 44 | 94.8  | 2.8 | 853    | 13 US-10-027-632-157095 | Sequence 157095,   |
| 45 | 94.8  | 2.8 | 853    | 13 US-10-027-632-157096 | Sequence 157096,   |

## ALIGNMENTS

RESULT 1  
US-09-901-511-1  
; Sequence 1, Application US/09901511  
; Publication No. US20010049435A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Wu-Wong, Jinhyun R.  
; TITLE OF INVENTION: THE MYOSTATIN GENE PROMOTER AND  
; TITLE OF INVENTION: INHIBITION OF ACTIVATION THEREOF  
; FILE REFERENCE: 6542 US D1  
; CURRENT APPLICATION NUMBER: US/09/901,511  
; CURRENT FILING DATE: 2001-07-09  
; PRIOR APPLICATION NUMBER: US 09/329,685  
; PRIOR FILING DATE: 1999-06-10  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3435  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-901-511-1

Query Match 43.0%; Score 1459.2; DB 9; Length 3435;  
Best Local Similarity 72.7%; Pred. No. 1.7e-263;  
Matches 2472; Conservative 0; Mismatches 743; Indels 187; Gaps 38;

QY 1 TGCCTCCGAGGACATAGAGGTTCCAAATCCCGACATGAGAGAAACGCTTC 60  
DB 119 TTCTATCTGGGCGCTCAGAGAGTTTCATCATCTGCACGAGAGAAATAACTTA 178  
QY 61 TTGAATTTCTTGAGTACTTATATTCATTCATGCTGACCTCCGAA-----GATTGG 114  
DB 179 CTTAAATTTCTTCAGTTCTTCTTCACCAATTCATATCTGTTCTGTAGAGAAATTGATTAG 238

115 ATAGAGCTGACTCTCATTATTCACAGTGGTTATGTTCTACCCAACTACCTGCCACA-TGA 173  
 239 ATATAGCAATTCCTCCATTCATAGTATGTTATGTTCTATTAAGTCACTTGCCACACTGA 298  
 174 ATAAGTATTCCTGAACTGAGCCCTAGGGGAACTACAAAGTTAGATCCCGTCAAGCT 233  
 299 GTTAGCAAAATATGAACTATGTTCCAGAGGGGAAAAAGGGTTAGTTGAGCCCTG--- 355  
 234 CTGGTCAAGTTTGTGTTAACCATCATATAAATCCTGTTTGTGTCATTCCTGTTT 293  
 356 GTCAATACATTTACATCACCCAACTCAATATATTAACCTGTTTATGATGTTTGTGTTA 415  
 294 AAAATATCTTATTAATAGTACGCTAATCTTCAACATTTGGTTGACACCAAGG 353  
 416 CAATTA-CATTAATTAATATATGTTTCTTTCATTCATTAACCTGAACTACAGCCA---G 470  
 354 CCTATTAACTGAAAGCCCTGAATGAAGCTTACATTAACACACATGTTTCTATGAGA 413  
 471 CAGCACTATACTCAGGCTGAATGATGCTTATCTAGACA---TGATTTTTCATGAG 527  
 414 AAAATTTTCTTCACTGCTCCGACAGCTTCTGCTTAAATTTGTGACAAATATACA 473  
 528 AACTTTTCCCTTAGGCAATACAGCCTT-----TTAAATTTGTGTAATATACACA 582  
 474 TAACATGAACTGACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 533  
 583 ACATTTAGCA-----TCTTAACATTTTAAAGTTTAAAGTTTAAAGTTTAAAGTTTAA 633  
 534 CACTTACCTTCTGCTGTAAGTATGATCAACATTCATCTTAGAACTTTTGTATCTTCTG 593  
 634 CATTCACACTGTTGTATGTAACATCAACCAATTCATCTTCAAAATTTTTCATCTTCCA 693  
 594 AATTGAAAATCTGCTATGTTGACAGTACTTCCCTCACTACACCGCACCTTCTC 653  
 694 GACTG-AAACTCTGATCTATCAACAGTAACTACCCCTCA-----GTGCTCAC 743  
 654 CAGCCCCCGGACACCATCTTCTTCAATGACATCTCTGCTGCTAGAAACA--- 710  
 744 CAGTCTCTGGCAACACCATGCTACTTTCATTCAGCTTCTCTGTATGTAAGAACATAG 803  
 711 -----CAGCCCTTCAACACTACCTGCTGGGGGCACTGT---AAGCAACAGATC 756  
 804 GAAACACAGCAGACGTCAGACATATGCTGGGGCCATTTTAAAAAGCAAAATCAAT 863  
 757 ACTCCCTACCGCCACCAATATGACACAAATATATAAAGCATGCTGCAATTCATGCTC 816  
 864 AAGAGAGCAATTAATAAAGAAAGCAAAATATGTAAGAAACATGACCTAAATAGACGG 923  
 817 AAAAGGGTGTGCT--AAGTATAGGGCTGAAC---AAGGACAGAAATGACTAGT 871  
 924 AAAAAGGGAATTTGTTTATGATAGAGCTGAAACAAAAGGCGAAACCTGCTTGT 983  
 872 TGACCTCAGCTGGGATCTGTGTGTGG--AAGCTCAAAATTTTCATTTGTTCTGTGAT 929  
 984 TGACCTCATCTGGGAACCTGTGCTCAATAGACTCAAAATTTTTCGCGCTGTGAT 1043  
 930 ACGCAAAATGCTTATAAAGCATGTAAGATTAATTAAGATTAATTAATTAATTAAT 989  
 1044 GCCACGATGACTAAAAA---TGCTAGGAATATGATTTCAATAGTAATTAATTTAGC 1099  
 990 CAAGCATTAATGTCAGACAGGATCATGATTAACAGACAGTACAT--GTGAAA 1047  
 1100 AAGTGGCAATTTTGTGATTAAGAAATCATAGAAATATGATATGATGTTGTTAGGGA 1159  
 1048 TGATATCTTTGTTCTTTATTTCAAGGAGTAAAGAAAGCGC-----T 1093  
 1160 TGACAACTTTGTTTCACTTTTTCAGAGTATTAAGAAATTAAGAGCTGAAATGTTGT 1219  
 1094 CACAGGCTGCTTACACATTTTACTAGAGAGCTAGCTATGCTAGCTGG----- 1144  
 1220 AACCTGCTGCTTGAATAATTTTACTTCTACAGGCTTAGAAAGTGGCTTTGTGAC 1279

1145 ---TAGTGGCAATTAACAACTGAAGCAGTTTATGTTCATGTGAGAGATTTAAACA 1201  
 1280 TGATTAATGGCAGCTATGACCTGAAGCAGTTTATGTTTCAATGTGAGAGCATTAATTAAGCA 1339  
 1202 TAATCTCAACCCCTCTGCTATGAACAGAGACTAAGTACCAAGTCCCAATTAATGCTCA 1261  
 1340 TAAATCTCAACCCCTCTGCTATGAACAGAGACTAAGTACCAAGTCCCAATTAATGCTCA 1399  
 1262 CTTACTATATGACAGGCACTGACTCAACATTTTACATGATTAATTAATTAATTAATTAAT 1321  
 1400 CTTACTATATGACAGGCACTGACTCAACATTTTACATGATTAATTAATTAATTAATTAAT 1459  
 1322 CAACACTCTATGAGAAAGCTGAAGTTAG---AAGTATCTCATTCATTAATTAACA 1376  
 1460 CAAAACCTTATGAGAAAGCTGAAGTTAGGAAAGTTAGTATCTCATTCATTAATTAACA 1519  
 1377 GT-----GGCAACTGAGATCTGAACCTCAGTCTATCACTCCAGAGACCTGAGATC 1428  
 1520 GTTAGAAGTGGCAAAAGTTGAGATTTGAACCTCAGTCTATCTGACCTCAGAGCTGAGTTC 1579  
 1429 CCAATGCTACACAAATCTATCAAGTTAAAGGAAAGAAAGATTTGATTTGCTCAGAG 1488  
 1580 TCAATTTCACTGCTATCAATCTTCAACATTAATTAATTAATTAATTAATTAATTAATTA 1639  
 1489 TGATAGGGGCAATATGTTACA---ATTATTAATTAACAAAGTTTATATGTTAAATA 1545  
 1440 TGATATGATGATGATGTTAACAATGATCATTAACATTTGAAAGATTTTACATTAAGAAATG 1699  
 1546 AATTATCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1605  
 1700 AATTATCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1759  
 1606 ATCTGAATCTCTGAGGCACTGCTGTTGTGTGCTGTTTCTTAACTTTAATGATGG 1665  
 1760 ATCTGAATCTCTGAGGCACTGCTGTTGTGTGCTGTTTCTTAACTTTAATGATGG 1818  
 1666 CAATCTTAATGATTAATGTAAGCCA-TTTTTTCTCAAGAGATGATTAATCTTTAAGA 1724  
 1819 CAATCTTAATGATTAATGTAAGGCCATTTTCTCAAGAGATGATTAATCTTTAAGA 1878  
 1725 AATTGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1784  
 1879 AATTGATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1938  
 1785 GTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1841  
 1939 GTAATTAATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1998  
 1842 ACCACTGACTCTCTTGG-GGAAAAAAGTAATGATTAATCTCTTGAAGTCTTGAAGT 1900  
 1999 GCCACTGATCTCTTGGAAAAAAGTAATGATTAATCTCTTGAAGTCTTGAAGTCTTGAAGT 2058  
 1901 TCCCAAAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1960  
 2059 TCCCAAAAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2118  
 1961 CTGCTATTAATTTGATGTTTAAATGATTAATTAATTAATTAATTAATTAATTAATTAAT 2020  
 2119 CTGCTATTAATTTGATGTTTAAATGATTAATTAATTAATTAATTAATTAATTAATTAAT 2178  
 2021 CTAAAGTTGAGATTTGATTCCTTACAGAGGCACTTCAATTTAGAAACAAAGGCCCA 2080  
 2179 CTAAAGTTGAGATTTGATTCCTTACAGAGGCACTTCAATTTAGAAACAAAGGCCCTTA 2238  
 2081 TTCTGTGCTCCCAAGCTTAAACCAAAATCCCTGCAAGTGTCTGCGCTCGGTCAAATGA 2140  
 2239 TTCTGTGCTCCCAAGCTTAAACCAAAATCCCTGCAAGTGTCTGCGCTCGGTCAAATGA 2298  
 2141 GAAATGSCAAAGAACTAGAGGTGCAACAGTACAGTAAAGTAAGTAAGTAAGTAAGTAAG 2200  
 2239 ACAAATTTGCAAAAGGGGTGCAACA-----TA 2325  
 2201 GCAACTACTAGAAAGCAAAAAATGGGACCTTCAATGATGATGTTCTTCCCTTCT 2260

Db 2326 TCGCGATTTGGGAAACAACAAAGTCACCCCTTTATCATGATCTCTCTCTTTAT 2385  
Qy 2261 GTGTTCAATGCTCCGATATATATTTACAGAGGGTAGATA-----ACATATTTT 2312  
Db 2386 GTGCTCATATATTTCTGATATATATTTATAGAAATAGATCTGCACTTTTATCTCTGG 2445  
Qy 2313 TCTTTTACACTGGAAGGCTGAGAAAATTGTTACCATCATATAAATTCATATCTTC 2372  
Db 2446 ATATTTACTGCTGAAATCTGAGGCAACTGTAATATCTCGCATGCAAGTTATAAA 2505  
Qy 2373 TAAGCATCTATGTTATTTCTAAG------TCAATAGCTGACATATCTCTTTGA 2426  
Db 2506 TTCAATTAATCTAGCTATGTTCAAGATTTTCTAATGCTGGCAATCCCTCTTGTA 2565  
Qy 2427 TAAACAATGAAAAACATCTCTGAGCAATATATATCTGCACTTTAGATAGTAGT 2486  
Db 2566 TAAACATAG-AAAAACATCTCTGAGTTATGTTAATCTGATCTTTAGAAATAGAA-- 2622  
Qy 2487 AACTTAATCTAGTCAATTTGAACTGAATACATTTTCAATGATGAATAAGATAT--- 2542  
Db 2623 ---ATAATGACATCTGACAAAGTTCAATATTTTCAATATTAATAAGACATGAA 2679  
Qy 2543 -TATTTAAAGTATTCATGACATTAATAATTA-AAGTAGATTTTCATATGCTT 2600  
Db 2680 CTATGTAATAAATATTCATGACATATGTTATATTAACATGACTTCAATATTTACT 2739  
Qy 2601 AAGATTTATTCAGGGAACAAGTTCTCAATTTATACAGAAAATCTTTACTGATC 2660  
Db 2740 AAGATTTATGTC-AAAAACAAGTTCTCAATATTAATGAATAATTTCAATGATATC 2798  
Qy 2661 AAGCTCTTTTCAATTAAGTC-TTCTGATTAATCTGATTTTCAATTTATACAGATA 2719  
Db 2799 ATATATCTTAATCTTTAATTCAGGCTTCTCTATTTTATTTTCCATTTACTGSCACTA 2858  
Qy 2720 AAAATTAATTTAATTAACAATAAATTAATTTT-TACTTCAATGCTTCTTAATAGTA 2778  
Db 2859 AAAATTAATTTAATTAACAATAAATAATTTTCTAATTTCAATTTCTGCTCAACATA 2918  
Qy 2779 TAAATCTTTTATTTTCTGAGGGAAGCAATCACTTTTATGATGAAGTAAAT 2838  
Db 2919 TAAATCTTTTATTTTCTGAGGGAAGTAAATTTT-ATATTTAATAATGATGAAT 2977  
Qy 2839 TAAGATTTATCTTAATTAATAATTTTAAAGTTTCAATATTAAGATTAAGATC 2898  
Db 2978 TAAATCTTATTTAATTAATTAACAATTAAGATGATGAGATTAAGATTAAGATC 3037  
Qy 2899 TAAGTATATGTTATTTTAAATGTTTAAATTTTTCGATGTCATACAGCTTT 2958  
Db 3038 ---AGTTATATTAATGCAACATGACCTTTTCAATGTTTCAATATCTTTT 3093  
Qy 2959 ATTAATCTATATTTATCTTTTAAAGATGATCAATTAAGATCACTTCTGATG 3018  
Db 3094 ATTAATTTGATATTAATTTCTTTTAAAGATGATCAATTAAGATCACTTCTGATG 3153  
Qy 3019 TAAACAATATCTTTGTTGTTGTTGTTGTTGTTTAACTCTGACAGGAGAT 3078  
Db 3154 TAAACAATATCTGTTGTTGTTGTTGTTGTTGTTGTTTAACTCTGACAGGAGAT 3213  
Qy 3079 CATTTGAGCAAGAGCAATCAAGATCCGAGCACTTGTCTCATCAAAAGTTGAT 3138  
Db 3214 CATTTGAGCAAGAGCAATCAAGATCCGAGCACTTGTCTCATCAAAAGTTGAT 3273  
Qy 3139 ATAAAGGCACTTGAATTAAGATTAATAAGATTAAGATTAAGATTAAGATTAAGAT 3198  
Db 3274 ATAAAGGCACTTGAATTAAGATTAATAAGATTAAGATTAAGATTAAGATTAAGAT 3333  
Qy 3199 ACTGGGAGGCAATTAAGATTTGTTGTTGTTGTTGTTGTTTCAAAAGGAAAGTAAAG 3258  
Db 3334 ACTGATATGATTAATTTTGTGTTGTTGTTGTTGTTGTTTCAAAAGGAAAGTAAAG 3393  
Qy 3359 AAGATTAAGCAAGGAAAGATTTGATTAATTTTAAACC 3300

Db 3394 AAGAAACAAGAAACAAAAAGATTAATGATTTTAAATC 3435  
Query 2  
US-10-610-473-1  
; Sequence 1, Application US/10610473  
; Publication No. US20040030114A1  
; GENERAL INFORMATION:  
; APPLICANT: Findlay, Robert  
; TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AN  
; TITLE OF INVENTION: METHODS FOR ITS USE  
; FILE REFERENCE: PCI0448A  
; CURRENT APPLICATION NUMBER: US/10/610,473  
; CURRENT FILING DATE: 2003-06-30  
; PRIOR APPLICATION NUMBER: US/09/626,959  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 60/146,540  
; PRIOR FILING DATE: 1999-07-30  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 2482  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-610-473-1  
Query Match 15.5%; Score 525; DB 17; Length 2482;  
Best Local Similarity 61.5%; Pred. No. 2.8e-88;  
Matches 1256; Conservative 0; Mismatches 665; Indels 122; Gaps 21;  
Qy 1188 GATGAATTTTAAACATTAATCTCAACCCCTGATGAAACAGACATTAAGTCAAGTA 1247  
Db 521 GAACACTGTGAGATTAATTTGAAAGTAAAGGCTTGAACAAAGCAAGCCCTTCTGCT 580  
Qy 1248 CCACTTACGCTCTTACTATATG-----ACAGCACTGATCTCAATTTACT 1299  
Db 581 TCAAGTATTAATTTCTATGAAAGGACTACATTTAGCTTATATTTGCTAAATTAAT 640  
Qy 1300 GTATTAATTAATTAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1359  
Db 641 GCTCAACCCCTTTAGTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 700  
Qy 1360 TCATTCATTTATTAACAGTGGCAACCTGAGATCTGAATCTGATCTCACTCCAGGA 1419  
Db 701 TGTATGACTTAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 760  
Qy 1420 CTTGATCCCAATTTGCTACCAATTTCTATCAAGTTAAAGGAGGAGGAGGAGGAGG 1479  
Db 761 TCTGAGCTCAAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 816  
Qy 1480 GCTCAGAGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1536  
Db 817 CTTGAGGATTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 876  
Qy 1537 TGAATAATTAATTTATCAACCAATTAATTAATTTTAAAGCTGATCTATATCTGCCA 1596  
Db 877 AGAAATTAATTTTCCAGCAAAATGATCTTATAGCCCTCTAATATATGCTTGTGA 936  
Qy 1597 ACAAGAATATGAAATCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1656  
Db 937 --TAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 994  
Qy 1657 AATGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1711  
Db 995 AATGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1054  
Qy 1712 ATACCTTTAAGATTTGATGAATAATGATTAATCTTTTCAAGGCTGATGATTTGA 1771  
Db 1055 ATGCTCTTAAATTTGATGAATAATGATTAATCTTTTCAAGGCTGATGATTTGA 1114  
Qy 1772 GTGCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1828  
Db 1115 GTTCACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1174

```

QY 1829 ATATTGATATGACCACTGACCTCTCTGGGG-----AAAAAGTATGATTAAC 1880
DB 1175 ATATTATATCAAGCCACACATAGTCTCTGGGGTGTGTGTAAGGGAGATGATTAATA 1234
QY 1881 TCTCTAGAGTCTTACCTTACCTTCCCAAAAGTAGAGAAAAATTAATCTCTGTGGCTG 1940
DB 1235 ATCTTAAGACTCTCTACGCTTCCCAACAGAGAGAGAA-----CTCTGTGGCTG 1285
QY 1941 GAAACAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2000
DB 1286 GAAACGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1343
QY 2001 AGACCTTGTGGCTCCCAAGTAGTGAAGTTGATTCCTTCAAGAGGCACTTCAAT 2060
DB 1344 CGATCTTGTGGCTCTTAAGCCAAAGGTGAAGTTGATTCCTTCAAGAGGCACTTCAAT 1403
QY 2061 TTAGAGAACAAAAGCCCATTTCTCTGCTCCAGACCTTACCCCAATCCCTGCGAGGTG 2120
DB 1404 TCAGAGAACAAAAGCCCATTTCTCTGCTCCAGACCTTACCCCAATCCCTGCGAGGTG 1462
QY 2121 TCTGCCCCGCTGCAATGAGAACTGGCAAGAGAACTAGAGAGTGCACAGTACTA 2180
DB 1463 TCTGCCCCGCTGCAATGAGAACTGGCAAGAGAGTGCAGTACTA----- 1518
QY 2181 GGAAGTAGAAAAAGTACACACTACGAGAGAGAGAAAGTGGGCACTTCAATGA 2240
DB 1519 -----GGGAGAGCAACAAAGGACCCCTTCA 1547
QY 2241 TGTGTTCTCTTCCCTTCTCTGTTGACAGATGCTCCGATATATTTACAGAGGTAGATA 2300
DB 1548 ---TGGCATCTTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1603
QY 2301 ACTACATTTTCTTCTTCAACACTGGAAGGCTGAGAGAACTTTTGT-----CCC 2351
DB 1604 ---TTGCACTTACTGTCAGCCCTGGAAGTGTGATCAAACTGAATATGCTCCAGGCG 1660
QY 2352 ATCAATAAATCACATCTCTCTGACCTCTCTGATTTTCTTAAGATCAAAATAGCTGACA 2411
DB 1661 TACTTACAAAATTCATATCTCTCTGAGCTGAGTACAGAGCTGCTCTCTCTGAGACA 1720
QY 2412 ATATCTCTTGTGTATTAATAACATGAAAAACATCTCTGAGCAATATTAATCTGCAAC 2471
DB 1721 GGATCTCTGTGCACTCAAAAAAAGAAAAAAGAAAAAGAACATCTGATCTTGT 1780
QY 2472 TTTAGAGTAGAGTAACTTAATCTAGTCAATTGAACTGAATACATTTTCTATGA 2531
DB 1781 ATCTCTGTAATGAAAAATGACAACTTAATAGCTGAATCAAGCAAGTTTTATGTTA 1840
QY 2532 ATTAAGATATTAAT-----TTAAAGTAAATTCATGAGCAATTAATTAATTAAGTA-GGAT 2586
DB 1841 GTCAAAAGCCATTAAGCTATCAAAAGTAAAGCCATGACAGAAAGCTGCCAGACTGCT 1900
QY 2587 TTTCAATATGTTGTAAGATTTATTCAGGAAACAAGTTCTCAATATTAATGACAGAAAT 2646
DB 1901 TTGTAATATGCTCTGACAAATAGCCATTAAGAAACAAGCTCTCAATATTAATGACACT 1960
QY 2647 CTTTACTAGTATCAAGTCTTTTCAATTAAGTCTTCTGAAATTAATCTGTAATTTCTTA 2706
DB 1961 TTTTAGCAGGGTCAACAACTGAGCTTTCTTAATTAATGCTGAGCTCTTCTGATTTTAC 2020
QY 2707 TTATACAGAGCTAAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2766
DB 2021 TTTCT-----CTAATTAACCGACCTTAAGCAATTTTCTCTCAATATTA 2068
QY 2767 ACTTAATATGTAATTAATTAATTAATTTCTGAGGAAAGCAATCACTTTTAAAGTA 2826
DB 2069 GTTTTAGTAAACAAACAGACCTCAAGTCAAAAGATTAATTAATTTCTTA-TTTTAAACA 2127
QY 2827 TGAAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2886
DB 2128 CAAATATCTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2180

```

```

QY 2887 ATGAATAGATCTAAGTATATGTAATGTAATTAATTAATTTTATTTTCCATGTCA 2946
DB 2181 ATTAATAGCTTAAGTACAGTATTAATTAATGTAATTAATTAATTAATTAATTAATTA 2239
QY 2947 CATACAGCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3006
DB 2240 CATATATCTTCAATGATTTGGGATTAATTAATTAATTAATTAATTAATTAATTAATTA 2299
QY 3007 CACCTTGACTGTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3066
DB 2300 TGCCCTGACTGTAAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2359
QY 3067 GACAGCAGATTCATTTGTGAGAGAGAGCAATACAGATCCGAGACACTTGTCTCAT 3126
DB 2360 GACAGCAGATTCATTTGTGAGAGAGAGCAATACAGATTCGAGACACTTGTCTCTCT 2419
QY 3127 CAAGTTGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3186
DB 2420 CTAAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2479
QY 3187 GTT 3189
DB 2480 GTT 2482

```

```

RESULT 3
US-10-251-115-54
; Sequence 54, Application US/10251115
; Publication No. US20030129171A1
; GENERAL INFORMATION:
; APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique
; TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMALS
; FILE REFERENCE: 52836/00016
; CURRENT APPLICATION NUMBER: US/10/251,115
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 08/891,789
; PRIOR FILING DATE: 1997-07-14
; PRIOR APPLICATION NUMBER: 09/007,761
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: PCT/IB98/01197
; PRIOR FILING DATE: 1998-07-14
; NUMBER OF SEQ ID NOS: 54
; SEQ ID NO 54
; LENGTH: 5790
; TYPE: DNA
; ORGANISM: bos taurus
US-10-251-115-54

Query Match      15.0%; Score 508.6; DB 15; Length 5790;
Best Local Similarity 99.1%; Pred. No. 4.8e-85;
Matches 522; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 2864 TTTTAAAGTTTACATTAATTAAGATTAATTAAGATTAATTAATTAATTAATTAATTA 2923
DB 18 TATCAAGATTTACATTAATTAAGATTAATTAAGATTAATTAATTAATTAATTAATTA 77
QY 2924 AGTTTAAATTTTGCATGTCACATTAAGCTTATTAATCAATGATTAATTTTCTTTA 2983
DB 78 AGTTTAAATTTTGCATGTCACATTAAGCTTATTAATCAATGATTAATTTTCTTTA 137
QY 2984 AGAATGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3043
DB 138 AGAATGATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 197
QY 3044 TGACAGACAGGTTTAACTTCTGACAGAGATTCATTTGTGAGACAGAGCAATCA 3103
DB 198 TGACAGACAGGTTTAACTTCTGACAGAGATTCATTTGTGAGACAGAGCAATCA 257
QY 3104 GATCCGAGACACTTGTCTCATCAAGTTGGAATTAATTAATTAATTAATTAATTAAT 3163
DB 258 GATCCGAGACACTTGTCTCATCAAGTTGGAATTAATTAATTAATTAATTAATTAATTA 317

```





```

Db      987 TAATACGCTAATTAATTGAGAACTGTTTCTCTCACTAATTTCTAGTACATATGAAA 928
Qy      2785 CATTTATTTCTGAGGAGAAAGCATATCACTTTTAAGTAGAGTAAATTAAGAT 2844
Db      927 TCATCTATTAATCTGTATATATACATGAGATTAATTTAAATATATCTTTATTCAG 868
Qy      2845 TTATTCATTAATTAATTAATTTTAAGTTTCACTAATTAAGATTAAGATTAAGT 2904
Db      867 TGAATAATGCTGCTAGTTTCACTGATTTTCTCTAATCTTAAGTTGCAATTAATTT 808
Qy      2905 TATATGTTATTTGTTAATAAGTTTAAATTTTTCAGATGTCATACAGCCTTTATTAAT 2964
Db      807 GCTCAGAGAGATGTTTCTTTTCAATGTTATATACCAAGAGATTAATGCAATTTATTAAT 748
Qy      2965 CATGATTTATTTCTTTTAAAGAGTAGTCAATGATCACTCACTGATCACTGATCA 3024
Db      747 TGTGATTTATTTCTTTTATGAGTAGTCAATGATCACTCACTGATCACTGATCA 688
Qy      3025 AATATCTGTTGCTGATGTCAGACAGAGGTTTAACTCTGACAGGAGATTCATTT 3084
Db      687 AATATCTGTTGCTGATGTCAGACAGAGGTTTAACTCTGACAGGAGATTCATTT 628
Qy      3085 GAGACAGAGGCAATCAAGATCCGAGACAGACTGTTCTCATCAAGTTGAGATTAATA 3144
Db      627 GAGACAGAGGCAATCAAGATCCGAGACAGACTGTTCTCATCAAGTTGAGATTAATA 570
Qy      3145 AGCCACTTGGAAATACAGTATAAAAGATTCACTGTTGAGCAAGTTGTTCTCAAGCTGG 3204
Db      569 AGCCACTTGGAAATACAGTATAAAAGATTCACTGTTGAGCAAGTTGTTCTCAAGCTGG 510
Qy      3205 CAGCATTAATGCTTGGCTTGGCTTACTCAAAAGCAAAAGATTAAGAGAAAGT 3264
Db      509 CAGCATTAATGCTTGGCTTGGCTTACTCAAAAGCAAAAGATTAAGAGAAAGT 455
Qy      3265 AAGAAACAAGGAGAAAGATTTGATTTGATTTAAACATGCAAAATCTGCAATCTGTT 3324
Db      454 AAGAAACAAGGAGAAAGATTTGATTTGATTTAAACATGCAAAATCTGCAATCTGTT 395
Qy      3325 TATATTTACCTATTATGCTGATGTTG 3352
Db      394 TATATTTACCTATTATGCTGATGTTG 367

```

RESULT 6  
US-10-027-632-120231  
; Sequence 120231, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218, 006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198, 676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193, 483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185, 218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167, 363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156, 358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146, 002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 120231  
; LENGTH: 942

```

; TYPE: DNA
; ORGANISM: Human
US-10-027-632-120231
Query Match      6.6%; Score 224.8; DB 13; Length 942;
Best Local Similarity 63.5%; Pred. No. 3,9e-32;
Matches 589; Conservative 1; Mismatches 258; Indels 80; Gaps 13;

```

402 TTTCTATGAGAAATTTTCTCTGAGTCTGTCAGACAGGCTTCTTGAATTTGTCG 461  
14 TTTTATATGAGAACTTTTCTCTGAGTCTGTCAGACAGGCTTCTTGAATTTGTCG 68  
Qy 462 ACAAAATATACATTAACATGAACTGACTATATTAATTAATTAATTAATTAATTAAT 521  
Db 69 TAAATATACACACATTTAGCA-----TCTTAACATTTTATAGTGTACAGTTGG 119  
Qy 522 TGGCATTAAGTACACTTACCTTGTGTGGAACATTAATTAATTAATTAATTAATTAAT 581  
Db 120 TGGCATTAAGTACACTTACCTTGTGTGGAACATTAATTAATTAATTAATTAATTAAT 179  
Qy 582 TTGATCTTCTGAAATGAAATCTGCACTATTTGATTAATTAATTAATTAATTAATTAAT 641  
Db 180 TTCACTTCTGAAATCTGCACTATTTGATTAATTAATTAATTAATTAATTAATTAAT 231  
Qy 642 GCACCTTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 701  
Db 232 --GTGCTCAACCACTGCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 289  
Qy 702 CTAGAAACA-----CAGCCTTCAACATTAATTAATTAATTAATTAATTAATTAAT 744  
Db 290 TTAGAAACATAGAAACAACAGCAGCAGTCACTGCTGCTGCTGCTGCTGCTGCTGCT 349  
Qy 745 AGCAACAGATCACTCCCTACCCGCAACCAATGACACAAATTAATTAATTAATTAATTAAT 804  
Db 350 AGCAAAATCAATTAAGAGAGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 409  
Qy 805 CATATCAATGCAAAAGGCTGCT--AAGTATAGAGGCTGAAC--AAGCAGAG 859  
Db 410 TAAATAGAGGAAAGGAAATTTGTTATAGTATAGAGCTGAACAAATTAATTAATTAAT 469  
Qy 860 AATGACTAGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917  
Db 470 CCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 529  
Qy 918 TGTCTGTCATGACCAAAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAAT 977  
Db 530 CCGCTGTCATGACCAAAATGCTTATTAATTAATTAATTAATTAATTAATTAATTAAT 585  
Qy 978 GATTAATCTGACCAAGATTAATGTCAGACAGGATTCATTAATTAATTAATTAATTAAT 1037  
Db 586 ATTAATTTTACCAAGTATGCAATTTGATTAATTAATTAATTAATTAATTAATTAAT 645  
Qy 1038 CAT--GTGGAATATATATCTTTGTTCTTATTAATTAATTAATTAATTAATTAAT 1092  
Db 646 TGTAGCGGAATATGCAACCTTTGTCATTTTCCAGGATTAATTAATTAATTAATTAAT 705  
Qy 1093 -----TCAAGGCTGCTTACACCAATTTTATTAATTAATTAATTAATTAATTAAT 1141  
Db 706 AACATGCTTTGTAACCTGCTGCTTATTAATTAATTAATTAATTAATTAATTAATTAAT 765  
Qy 1142 CGG-----TACCTGCAATTAACAATGAAAGCACTTATTAATTAATTAATTAATTAAT 1189  
Db 766 AGGCTTTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 825  
Qy 1190 TGAATTTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1249  
Db 826 TAAATTTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 885  
Qy 1250 AGTATGAGTCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1277  
Db 886 AGTATGAGTCACTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 913

```

RESULT 7
US-10-027-632-120231
; Sequence 120231, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIORITY FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 120231
; LENGTH: 942
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-120231

Query Match      6.6%; Score 224.8; DB 17; Length 942;
Best Local Similarity 63.5%; Pred. No. 3.9e-32;
Matches 589; Conservative 1; Mismatches 258; Indels 80; Gaps 13;

QY 402 TTTCATGAGGAAAAATTTTCTTCAGTCCCTGCACAGCCTTCCTGTTAAATTTGG 461
DB 14 TTTTATGAGGAACTTTTCCCTTAGGCAATACAGCCTT-----TTAAATTTGG 68
QY 462 ACAAAATATATACATATGAAAGTACTATTTAACTGATTTTAACTGATGAGTTGAG 521
DB 69 TAAATATATACACAACTTATGACA-----TCTTAACATTTTAAAGTGATGAGTTGG 119
QY 522 TGGATTAAAGTACTTAACTTCTGCTGGAATGATGATGATGATGATGATGATGATGATGAT 581
DB 120 TGGATTAAAGTACTTAACTTCTGCTGGAATGATGATGATGATGATGATGATGATGATGAT 179
QY 582 TTGATCTTCTGGAATGAAATCTGATCTATTTGACAGTATGATGATGATGATGATGATGATGAT 641
DB 180 TTGATCTTCTGGAATGAAATCTGATCTATTTGACAGTATGATGATGATGATGATGATGATGAT 231
QY 642 GCACCTTCTCTGCAAGCCCGGCAACCAATCTTCTTTCATGACAGTATGATGATGATGATGAT 701
DB 232 --GTGCTCAACCGAGTCCCTGGAACCAACATGCTACTTTCATTTGAGCTTTCTGTGA 289
QY 702 CTAGGAACA-----CAGCCCTTGAACATGATGATGATGATGATGATGATGATGATGATGAT 744
DB 290 TTAGGAACATAGGAACCAACGAGCAAGTATGATGATGATGATGATGATGATGATGATGATGAT 349
QY 745 AGCAACAGATCACTCCCTACCGCACCAATGACCAAAATATATAAAAGATGATGATGATGATGAT 804
DB 350 AGCAAAATCATATAGAGAGCAATATAAAAGAAAGCAAAATATATGAAACATGATGATGATGAT 409
QY 805 CATATGATGCAAAAAGGATGCTTGTCT--AAGTATGAGGCTGAAAC--AAGGCAAG 859
DB 410 TAAATATAGCGGAAAGGAAATTTGTTTATATGATGATGATGATGATGATGATGATGATGATGAT 469
QY 860 AATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 917
DB 470 CCTGCTGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529

```

```

QY 918 TGTTCGTGATACGACCAAAATGCTTATATAAGCATGATGATGATGATGATGATGATGATGAT 977
DB 530 CGCTCTGTAATGACAGGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 585
QY 978 GATTAATCTCAGCAAGATATATATGTCAGACAGGATCCATGATATACAGCACTGATC 1037
DB 586 ATAAATTTTACCAAGTGGCAAAATTTGATATACGAATATATATATATGAAATGATGATGAT 645
QY 1038 CAT--GTGGAATATGATATCTTTGTTTCTTATTTCCAGGAGTATGAGGAAGAGCGC--- 1092
DB 646 TGTTAGCGGAATATGACAACTTTGTTTCTTATTTCCAGGATGATGATGATGATGATGATGATGAT 705
QY 1093 -----TCAAGGCTGCTTACACCACTTTTATGAGAGTACGCTATGCTAGT 1141
DB 706 AACATGCTTGTATACCTGCTGCTTGTGAAATTTTACTTCTCAGAGGCTGAAAGT 765
QY 1142 CGG-----TAGCTGGCAATTAACAACTGAAAGCACTTCTAGTTCAATGAGAGA 1189
DB 766 AGGCTTTGTGATGATATATGAGCACTATGACCTGAAAGCACTTCTAGTTCAATGAGAGA 825
QY 1190 TGAATTTAACCATATATCTCAACCCCTCTGCATGAAACAGAGACTAAGTACTCAAGTACC 1249
DB 826 TAAATTTAAGCATATATCTCAACCCCTCTGCATGAAACAGAGCACTTCAATGATGCC 885
QY 1250 AGTTATCAGTCACTTACTATATGACAG 1277
DB 886 AGTTATCAGTCACTTACTATATGACAG 913

```

```

RESULT 8
US-10-366-345-27
; Sequence 27, Application US/10366345
; Publication No. US20030224501A1
; GENERAL INFORMATION:
; APPLICANT: Young, et al.
; TITLE OF INVENTION: Bone Morphogenetic Protein Polynucleotides, Polypeptides and
; FILE REFERENCE: PT189
; CURRENT APPLICATION NUMBER: US/10/366,345
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 2823
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-366-345-27

Query Match      5.6%; Score 190; DB 17; Length 2823;
Best Local Similarity 91.0%; Pred. No. 2.1e-25;
Matches 202; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 3168 AGATTCACTGCTGTCGCAAGTTGCTCTCAAGCTGGCAGGATTAAGTTGCTGGC 3227
DB 1 AGATTCACTGCTGTCGCAAGTTGCTCTCAAGCTGGCAGGATTAAGTTGCTGGC 60
QY 3228 GTTACTCAAAAGCAAAAGAAAGTAAAGAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 3287
DB 61 ATTACTCAAAAGCAAAAGAAAGTAAAGAAAGTAAAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 120
QY 3288 TGATTTTAAACATGCAAAATCTGTTATATATTTTAACTATTTATGATGATGAT 3347
DB 121 TGATTTTAAACATGCAAAATCTGTTATATTTTAACTATTTATGATGATGAT 180
QY 3348 TGTGCTGCGCCAGTGTGATGAAATGAGAACAGGACAGAA 3389
DB 181 TGTGCTGCTGTCAGTGTGATGAAATGAGAACAGGACAGAA 222

RESULT 9
US-10-610-473-3
; Sequence 3, Application US/10610473
; Publication No. US20040030114A1

```

GENERAL INFORMATION:  
APPLICANT: Findlay, Robert  
TITLE OF INVENTION: MYOSTATIN REGULATORY REGION, NUCLEOTIDE SEQUENCE DETERMINATION AND METHODS FOR ITS USE  
FILE REFERENCE: PC10448A  
CURRENT APPLICATION NUMBER: US/10/610,473  
CURRENT FILING DATE: 2003-06-30  
PRIOR APPLICATION NUMBER: US/09/626,959  
PRIOR FILING DATE: 2000-07-27  
PRIOR APPLICATION NUMBER: 60/146,540  
PRIOR FILING DATE: 1999-07-30  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 200  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-610-473-3

Query Match 5.1%; Score 174.4; DB 17; Length 200;  
Best Local Similarity 92.0%; Pred. No. 5.8e-23;  
Matches 184; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 2390 AGTCAATGATCAGCTCACCCTGACTGTAAACAATACTGTTGGTGTGACG 3049  
DB 1 AGTCAATGATCAGCTCACCCTGACTGTAAACAATACTGTTGGTGTGACG 60  
QY 3050 ACAGGGTTTAACCTCTGACACCGAGATTCTGTTGGAGCAGACCAATCAGATCCC 3109  
DB 61 ACAGGGTTTAACCTCTGACACCGAGATTCTGTTGGAGCAGACCAATCAGATCCC 120  
QY 3110 GACGACCTGTCTTCATGAAAGTTGGAATATTAAGACCACTGGAATACAGTATTAAG 3169  
DB 121 GACGACCTGTCTTCATGAAAGTTGGAATATTAAGACCACTGGAATACAGTATTAAG 180  
QY 3170 ATTCACTGTGTGGCAGTT 3189  
DB 181 ACTCCCTGGCGTGGCAGGTT 200

RESULT 10  
US-10-251-115-1  
Sequence 1, Application US/10251115  
Publication No. US20030129171A1  
GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique  
TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMAL  
FILE REFERENCE: 52836/00016  
CURRENT APPLICATION NUMBER: US/10/251,115  
CURRENT FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: US/09/482,573  
PRIOR FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: 08/891,789  
PRIOR FILING DATE: 1997-07-14  
PRIOR APPLICATION NUMBER: 09/007,761  
PRIOR FILING DATE: 1998-01-15  
PRIOR APPLICATION NUMBER: PCT/IB98/01197  
PRIOR FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 54  
SEQ ID NO 1  
LENGTH: 1196  
TYPE: DNA  
ORGANISM: Bos taurus  
US-10-251-115-1

Query Match 4.0%; Score 134.4; DB 15; Length 1196;  
Best Local Similarity 99.3%; Pred. No. 4e-15;  
Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3255 AGGAAGAGTAAGACAGGAGAAAGATTGTATGTTTAAACATGCAAAAAGTGA 3314  
DB 1 AGGAAGAGTAAGACAGGAGAAAGATTGTATGTTTAAACATGCAAAAAGTGA 60

QY 3315 AATCTGTTTATATTACTTATTATGCTGATTTGCTGGCCCACTGATCTGAATGA 3374  
DB 61 AATCTGTTTATATTACTTATTATGCTGATTTGCTGGCCCACTGATCTGAATGA 120  
QY 3375 GAACAGGAGCAGAG 3390  
DB 121 GAACAGGAGCAGAG 136

RESULT 11  
US-10-251-115-3  
Sequence 3, Application US/10251115  
Publication No. US20030129171A1  
GENERAL INFORMATION:  
APPLICANT: Grobet, Luc; Georges, Michel; and Poncelet, Dominique  
TITLE OF INVENTION: MUTATIONS IN THE MYOSTATIN GENE CAUSING DOUBLE-MUSCLING IN MAMMAL  
FILE REFERENCE: 52836/00016  
CURRENT APPLICATION NUMBER: US/10/251,115  
CURRENT FILING DATE: 2002-09-20  
PRIOR APPLICATION NUMBER: US/09/482,573  
PRIOR FILING DATE: 2000-01-13  
PRIOR APPLICATION NUMBER: 08/891,789  
PRIOR FILING DATE: 1997-07-14  
PRIOR APPLICATION NUMBER: 09/007,761  
PRIOR FILING DATE: 1998-01-15  
PRIOR APPLICATION NUMBER: PCT/IB98/01197  
PRIOR FILING DATE: 1998-07-14  
NUMBER OF SEQ ID NOS: 54  
SEQ ID NO 3  
LENGTH: 1240  
TYPE: DNA  
ORGANISM: Bos taurus  
US-10-251-115-3

Query Match 3.9%; Score 132.8; DB 15; Length 1240;  
Best Local Similarity 98.5%; Pred. No. 8e-15; 2; Indels 0; Gaps 0;  
Matches 134; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3255 AGGAAGAGTAAGACAGGAGAAAGATTGTATGTTTAAACATGCAAAAAGTGA 3314  
DB 1 AGGAAGAGTAAGACAGGAGAAAGATTGTATGTTTAAACATGCAAAAAGTGA 60  
QY 3315 AATCTGTTTATATTACTTATTATGCTGATTTGCTGGCCCACTGATCTGAATGA 3374  
DB 61 AATCTGTTTATATTACTTATTATGCTGATTTGCTGGCCCACTGATCTGAATGA 120  
QY 3375 GAACAGGAGCAGAG 3390  
DB 121 GAACAGGAGCAGAG 136

RESULT 12  
US-09-854-867-233  
Sequence 233, Application US/09854867  
Publication No. US20030224356A1  
GENERAL INFORMATION:  
APPLICANT: JOAN, KNOLL, H  
TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING  
FILE REFERENCE: 30307  
CURRENT APPLICATION NUMBER: US/09/854,867  
CURRENT FILING DATE: 2003-05-08  
NUMBER OF SEQ ID NOS: 613  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 233  
LENGTH: 653  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: repeat region  
LOCATION: (1)..(653)  
OTHER INFORMATION: mer82

```

; NAME/KEY: misc feature
; LOCATION: (186)..(187)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (544)..(544)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (557)..(557)
; OTHER INFORMATION: n is a, c, g or t
; NAME/KEY: misc feature
; LOCATION: (567)..(567)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-233
```

Query Match 3.7%; Score 126.2; DB 10; Length 653;

Best Local Similarity 70.9%; Pred. No. 1.1e-13;

Matches 222; Conservative 1; Mismatches 81; Indels 9; Gaps 4;

```

Oy 119 AGTGAAGCTGATTAATTCAGAGTGGTTATGTTCTAACCAATCACTGCCAACA-TGAATPA 177
    |||||
Db 2 AGTTGATTCCTAATTAATTCAGAGTGGTTATGTTCTAAAGTCAACGCGAAGCACTGAATTA 61

Oy 178 GTGATTCCTGAACCACTGCCCTAGGGGAACTACAGAGTTAGTCCGTCAGCCTCTGG 237
    |||||
Db 62 GCGAATCTGAACCACTGCCCTAGAGGAATACAGATTAGTTCCTGCAAGCCTCTGG 121

Oy 238 TC---ACGTTTGTGAACCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTA 294
    |||||
Db 122 TCACAACTTTTCATCAACCATCATATATATATATATATATATATATATATATATATATTA 181

Oy 295 AAATATCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 354
    |||||
Db 182 AGACNMC-TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 238

Oy 355 CCTATTACTGAAGCCCTGAATGAAGTTACATTAACACATTTGTTTCTATGAGGA 414
    |||||
Db 239 --CACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 296

Oy 415 AAATTTTCTTC 427
    |||||
Db 297 CATCAAGCCTTC 309
```

#### RESULT 13

US-10-786-970A-233

; Sequence 233, Application US/10786970A

; Publication No. US2005006449A1

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOUL

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/10/786,970A

; PRIOR FILING DATE: 2004-02-24

; PRIOR APPLICATION NUMBER: US/09/573,080

; PRIOR FILING DATE: 2000-05-16

; NUMBER OF SEQ ID NOS: 479

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 233

; LENGTH: 653

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat\_region

; LOCATION: (1)..(653)

; OTHER INFORMATION: mer82

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: n is a, c, g or t

; PUBLICATION INFORMATION:

; PUBLICATION INFORMATION:

; AUTHORS: Jurka, J, Malichiewicz, J, Milosavljevic, A

; TITLE: Prototypic sequences for human repetitive DNA

; JOURNAL: Journal of Molecular Evolution

; VOLUME: 35

; ISSUE: 4

; PAGES: 286-291

; DATE: 1992-10-

; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)

; DATABASE ENTRY DATE: 1996-01-26

; DATABASE ENTRY DATE: 1996-01-26

US-10-786-970A-233

Query Match 3.7%; Score 126.2; DB 19; Length 653;

Best Local Similarity 70.9%; Pred. No. 1.1e-13;

Matches 222; Conservative 1; Mismatches 81; Indels 9; Gaps 4;

```

Oy 119 AGTGAAGCTGATTAATTCAGAGTGGTTATGTTCTAACCAATCACTGCCAACA-TGAATPA 177
    |||||
Db 2 AGTTGATTCCTAATTAATTCAGAGTGGTTATGTTCTAAAGTCAACGCGAAGCACTGAATTA 61

Oy 178 GTGATTCCTGAACCACTGCCCTAGGGGAACTACAGAGTTAGTCCGTCAGCCTCTGG 237
    |||||
Db 62 GCGAATCTGAACCACTGCCCTAGAGGAATACAGATTAGTTCCTGCAAGCCTCTGG 121

Oy 238 TC---ACGTTTGTGAACCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 294
    |||||
Db 122 TCACAACTTTTCATCAACCATCATATATATATATATATATATATATATATATATATATTA 181

Oy 295 AAATATCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 354
    |||||
Db 182 AGACNMC-TTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 238

Oy 355 CCTATTACTGAAGCCCTGAATGAAGTTACATTAACACATTTGTTTCTATGAGGA 414
    |||||
Db 239 --CACTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 296

Oy 415 AAATTTTCTTC 427
    |||||
Db 297 CATCAAGCCTTC 309
```

#### RESULT 14

US-09-859-211-13

; Sequence 13, Application US/09859211

; Patent No. US20020157125A1

; GENERAL INFORMATION:

; APPLICANT: Lee, Se-Jin

; TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-8

; FILE REFERENCE: 07265/144001

; CURRENT APPLICATION NUMBER: US/09/859,211

; PRIOR FILING DATE: 2001-05-15

; PRIOR APPLICATION NUMBER: 09/019,070

; PRIOR FILING DATE: 1998-02-05

; PRIOR APPLICATION NUMBER: 08/862,445

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 08/847,910

; PRIOR FILING DATE: 1997-04-28

; PRIOR APPLICATION NUMBER: 08/795,071

; PRIOR FILING DATE: 1997-02-05

; PRIOR APPLICATION NUMBER: 08/525,596

; PRIOR FILING DATE: 1995-10-26

; PRIOR APPLICATION NUMBER: PCT/US94/03019

; PRIOR FILING DATE: 1994-03-18

; PRIOR APPLICATION NUMBER: 08/033,923

; PRIOR FILING DATE: 1993-03-19

; NUMBER OF SEQ ID NOS: 51

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 2743

; TYPE: DNA

; ORGANISM: Homo sapiens

```

;      FEATURE:
;      NAME/KEY: CDS-
;      LOCATION: (59) ... (1183)
;      US-09-859-211-13

```

|                           |        |                    |           |              |
|---------------------------|--------|--------------------|-----------|--------------|
| Query Match               | 3.7%   | Score 126.2;       | DB 9;     | Length 2743; |
| Best Local Similarity     | 91.2%; | Pred. No. 1.9e-13; |           |              |
| Matches 134; Conservative | 0;     | Mismatches 13;     | Indels 0; | Gaps 0;      |

QY 3243 AAGGAAAAGTAAAGAGTAGAACAAGGAAAAGTTGATTGATTTTAAACCAT 3302  
 Db 1 AAGGAAAGTAAAGAGAGGAAACAAGACAGAGAAAAGATTATTTGATTTTAAATCAT 60

QY 3303 GCATAAATCTCGTTATATTACCAATTTCGTAATGTGCTGCGCCAGT 3362

Db 61 GCAAAACGCAACTCTGTTTATATTATACCGTTTATGCTGATGTGCTGCGCCAGT 120

|    |      |                             |      |
|----|------|-----------------------------|------|
| QY | 3363 | GGATCTGAATGAGAACAGCGAGCAGAA | 3389 |
|    |      |                             |      |
| Db | 121  | GGATCTAAATGAGAACAGTGAGCAAAA | 147  |

RESULT 15  
US-09-841

US-09-841-730-1  
; Sequence 1, Application US/09841730  
; Patent No. US20020157126A1

```

; GENERAL INFORMATION:
; APPLICANT: Lee, Se-Jin

```

1. APPLICANT: McPherron, Alexandra C.  
2. TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,  
3. FIELD OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF AND METHODS OF USING SAME

FILE REFERENCE: JHU1470-2  
CURRENT APPLICATION NUMBER: US/09/841,730

CURRENT FILING DATE: 2001-04-24  
 PRIOR APPLICATION NUMBER: 09/626,896

;  
; PRIOR FILING DATE: 2000-07-27  
; PRIOR APPLICATION NUMBER: 09/485,046

; PRIOR FILING DATE: 2000-01-31  
 ; PRIOR APPLICATION NUMBER: PCT/US98/15598

PRIOR FILING DATE: 1998-07-28  
PRIOR APPLICATION NUMBER: 60/054,461  
PRIOR FILING DATE: 1997-08-01

```

; PRIOR FILING DATE: 1557-08-01
; NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0

```

```

; SEQ ID NO 1
:
: LENGTH: 2743

```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
;

```

```

; FEATURE:
; NAME/KEY: CDS
;

```

| Query Match | 3.7% | Score 126.2 | DB 9 | Length 2743 |
|-------------|------|-------------|------|-------------|
|-------------|------|-------------|------|-------------|

| QY      | 3243 | AGAGAAAGTAAAGGAGAGTAAAGACAAAGGAAAGATGTTGATTTAAACCAT | 3302          |
|---------|------|-----------------------------------------------------|---------------|
| seqs    | 100  | 100                                                 | 100           |
| Matches | 134  | 0                                                   | Mismatches 13 |
|         |      |                                                     | Indels 0      |
|         |      |                                                     | Gaps 0        |

Db 1 AAGAAAAGTAAAGAGAAACAGAACCAAGAAAAGATTATATGATTTTAAATCAT 60

QY 3303 GCAAAACTGCAATCTCTGTTATATTAACTATTTATGCTGATGTGTCGCGCAGT 3365

Db 61 GCAAAACTGCACTCTGTATTATTACCC  
QY 3363 GGATCTGAATGAGACAGCGACGAA 3389

Search completed: March 31, 2005, 17:30:01  
Job time : 1241 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2005, 09:01:11 ; Search time 6894 Seconds  
(without alignments)  
18717.417 Million cell updates/sec

Title: US-09-743-312D-1\_COPY\_7103\_10492  
 Perfect score: 3390

Sequence: 1 **tgctgctcgaagccatag**.....**atgagaacagcgagcagaag** 3390

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

### Listing first 45 summaries

Database :

```

EST: *
1:  gb_est1: *
2:  gb_est2: *
3:  gb_hlc: *
4:  gb_est3: *
5:  gb_est4: *
6:  gb_est5: *
7:  gb_est6: *
8:  gb_gss1: *
9:  gb_gss2: *

```

**Pred. No.** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysts of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description         |
|------------|-------|-------------|--------|----|----------|---------------------|
| C 1        | 235.2 | 6.9         | 817    | 9  | CR273079 | Forward s           |
| C 2        | 235.2 | 6.9         | 829    | 9  | BX971880 | Forward s           |
| C 3        | 231.8 | 6.8         | 835    | 9  | CR242965 | Forward s           |
| C 4        | 218.6 | 6.4         | 615    | 9  | CR198021 | Forward s           |
| C 5        | 175.2 | 5.2         | 680    | 9  | AG325355 | Mus muscu           |
| C 6        | 119.6 | 3.5         | 628    | 6  | BY730292 | BY730292            |
| C 7        | 119.6 | 3.5         | 681    | 6  | BY730284 | BY730284            |
| C 8        | 117.4 | 3.5         | 704    | 8  | AQ424198 | CITR1-E1-           |
| C 9        | 111.8 | 3.3         | 749    | 1  | AUI20374 | AUI20374            |
| C 10       | 107.8 | 3.2         | 1101   | 9  | CNS00EVL | Al069706 Drosophi   |
| C 11       | 107.8 | 3.2         | 571    | 8  | B95505   | B95505 CIT-HSP-216  |
| C 12       | 107.2 | 3.2         | 440    | 8  | AQ759830 | AQ759830 HS_5430_A  |
| C 13       | 106.4 | 3.1         | 987    | 8  | CC118439 | CC118439 NDL_83G12  |
| C 14       | 104   | 3.1         | 487    | 8  | AQ103350 | AQ103350 HS_3010_B  |
| C 15       | 103.4 | 3.1         | 624    | 9  | AG124176 | AG124176 Pan trogl  |
| C 16       | 102.6 | 3.0         | 376    | 8  | AQ170583 | AQ170583 HS_2165_A  |
| C 17       | 101.4 | 3.0         | 1101   | 9  | CNS00EVL | Al069706 Drosophi   |
| C 18       | 100.6 | 3.0         | 311    | 8  | B92572   | B92572 CIT-HSP-217  |
| C 19       | 100   | 2.9         | 1391   | 9  | CG754863 | CG754863 P050-2-G0  |
| C 20       | 99.8  | 2.9         | 1092   | 9  | CNS02231 | AL175656 Tetradon   |
| C 21       | 98.4  | 2.9         | 810    | 9  | CC562231 | CC562231 CH240_473  |
| C 22       | 97.8  | 2.9         | 541    | 8  | AO701888 | AO701888 HS_5356_B  |
| C 23       | 97.8  | 2.9         | 798    | 1  | AV751702 | AV751702 AV751702   |
| C 24       | 97.6  | 2.9         | 918    | 8  | AZ543525 | AZ543525 ENTCC766TR |

|      |      |     |      |   |          |                     |
|------|------|-----|------|---|----------|---------------------|
| C 25 | 97.2 | 2.9 | 876  | 2 | BB601207 | BB601207            |
| C 26 | 96.8 | 2.9 | 303  | 2 | CNS00961 | AB053559 Drosophila |
| C 27 | 96.4 | 2.8 | 758  | 9 | CG925926 | IC925926 F085622Ba  |
| C 28 | 96.2 | 2.8 | 514  | 4 | BM688798 | BM688798 UI-E-CQ1-  |
| C 29 | 95.6 | 2.8 | 473  | 8 | B47307   | B47307 HS-1056-A1-  |
| C 30 | 95.6 | 2.8 | 725  | 7 | CK460720 | CK460720 931020 MA  |
| C 31 | 95.6 | 2.8 | 725  | 7 | CK461474 | CK461474 931788 MA  |
| C 32 | 95.4 | 2.8 | 360  | 8 | B67051   | B67051 C1F-HSP-201  |
| C 33 | 95   | 2.8 | 586  | 8 | BH051338 | BH051338 RPCI-24-3  |
| C 34 | 95   | 2.8 | 1101 | 9 | CNS00303 | AB064091 Drosophila |
| C 35 | 94.8 | 2.8 | 531  | 5 | BO272003 | BO272003 1k17d12.Y  |
| C 36 | 94.6 | 2.8 | 1877 | 9 | CR721531 | CR721531 Tetradodon |
| C 37 | 94   | 2.8 | 657  | 9 | AG068562 | AG068562 Pan. t1091 |
| C 38 | 93.8 | 2.8 | 795  | 5 | B0294111 | B0294111 6035577350 |
| C 39 | 93.4 | 2.8 | 632  | 8 | AQ285725 | AQ285725 RPCI11-89  |
| C 40 | 93   | 2.7 | 370  | 2 | BE156384 | BE156384 QVO-HT036  |
| C 41 | 92.8 | 2.7 | 833  | 8 | BZ599613 | BZ599613 WHAC1677F  |
| C 42 | 92.6 | 2.7 | 1101 | 9 | CNS00303 | AB064091 Drosophila |
| C 43 | 92.6 | 2.7 | 468  | 8 | AQ225066 | HA225066 HS.2017.A  |
| C 44 | 92.2 | 2.7 | 757  | 9 | CR827108 | CR827108 GR0AA5ED   |
| C 45 | 92.2 | 2.7 | 1364 | 9 | CG757966 | CG757966 F053-2-D0  |

## ALIGNMENTS

| LOCUS      | CR273079/c                                                                                                                                                    | 817 bp                                                                                                                              | DNA                | linear     | GSS 06-JUL-2004 |
|------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------|--------------------|------------|-----------------|
| DEFINITION | CR273079                                                                                                                                                      | Forward strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN334f11, genomic survey sequence. |                    |            |                 |
| ACCESSION  | CR273079                                                                                                                                                      |                                                                                                                                     |                    |            |                 |
| VERSION    | CR273079.1                                                                                                                                                    | GI:50051934                                                                                                                         |                    |            |                 |
| KEYWORDS   | GSS; genome survey sequence; MICEP.                                                                                                                           |                                                                                                                                     |                    |            |                 |
| SOURCE     | Mus musculus (house mouse)                                                                                                                                    |                                                                                                                                     |                    |            |                 |
| ORGANISM   | Mus musculus                                                                                                                                                  |                                                                                                                                     |                    |            |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 817)       |                                                                                                                                     |                    |            |                 |
| AUTHORS    | Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jokers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A. |                                                                                                                                     |                    |            |                 |
| TITLE      | Direct Submission                                                                                                                                             |                                                                                                                                     |                    |            |                 |
| JOURNAL    | Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <a href="http://www.sanger.ac.uk/MICEP">http://www.sanger.ac.uk/MICEP</a>       |                                                                                                                                     |                    |            |                 |
| FEATURES   | location/Qualifiers                                                                                                                                           |                                                                                                                                     |                    |            |                 |
| source     | 1..817                                                                                                                                                        |                                                                                                                                     |                    |            |                 |
|            | /organism="Mus musculus"                                                                                                                                      |                                                                                                                                     |                    |            |                 |
|            | /mol_type="genomic DNA"                                                                                                                                       |                                                                                                                                     |                    |            |                 |
|            | /db_xref="taxon:10090"                                                                                                                                        |                                                                                                                                     |                    |            |                 |
|            | /clone="MHPN334f11"                                                                                                                                           |                                                                                                                                     |                    |            |                 |
|            | /clone_11b="MHPN"                                                                                                                                             |                                                                                                                                     |                    |            |                 |
| ORIGIN     |                                                                                                                                                               |                                                                                                                                     |                    |            |                 |
|            | Query Match                                                                                                                                                   | 6.9%;                                                                                                                               | Score 235.2;       | DB 9;      | Length 817;     |
|            | Best Local Similarity                                                                                                                                         | 68.9%;                                                                                                                              | Pred. No. 5.4e-37; |            |                 |
|            | Matches 452;                                                                                                                                                  | Conservative 0;                                                                                                                     | Mismatches 168;    | Indels 36; | Gaps 8;         |
| QY         | 1370 TTACACAGTGGCAACTGAGATCGAATCGAGTCTATCCAACTCAGAGACTGAGATCC                                                                                                 | 1429                                                                                                                                |                    |            |                 |
| DB         | 639 TTAGAAAGGCAAAATTGAGATTGAATCTGAGTTTATTGACTCTTCAGTCTCAGCTCA                                                                                                 | 580                                                                                                                                 |                    |            |                 |
| QY         | 1430 CAATTGCTACCAATTTCTAATCAAGTTAAAGGAAAAAGATTGATTGCTCAGAACT                                                                                                  | 1489                                                                                                                                |                    |            |                 |
| DB         | 579 CAATGGCAGTTCAGTCTTAAAAAATCAAGATCA---ATTTCCTTGAGT                                                                                                          | 524                                                                                                                                 |                    |            |                 |
| QY         | 1490 GTATAGGGGCAATGTATAC---AATTAACTATCAAGATTATATGTGAAAAATTA                                                                                                   | 1546                                                                                                                                |                    |            |                 |
| DB         | 523 ATATAGCAGCATGTGATATGATATTATGATGACGAAAAAGATTCTATGCGAAAAATGA                                                                                                | 464                                                                                                                                 |                    |            |                 |
| QY         | 1547 ATTATATCAAACTAAATTAACCTTATTAAGCCTGATCTAATCTGCTCCGCAAAAGACTA                                                                                              | 1606                                                                                                                                |                    |            |                 |
| DB         | 463 ATTTTCAGCAAAATCTGACTTATATAGCCCTGCTCTAATTTGCTTTGTA--TAAAGG                                                                                                 | 406                                                                                                                                 |                    |            |                 |



|    |      |                                                              |      |
|----|------|--------------------------------------------------------------|------|
| Qy | 1607 | TCGGAATTCCTCAGGGGCACTGGTTGTGCTCGGTTTTCTTAATCTTTAATATAGGGC    | 1666 |
| Db | 405  | GCCAGATCACCTCAGGGGTGCTGGTGTGGTCTGGTTTCTTAATCTTTAATATAGGGC    | 346  |
| Qy | 1667 | AAATCTATGATTAATGTAAAGCCA-----TTTTCCTCAGAGATGAGATTAACCTCTTA   | 1721 |
| Db | 345  | AAATCTGTAACATTATGGAAGCCACTTTTTTTTCTCAGAGATTAATAGTGCCTCTTA    | 286  |
| Qy | 1722 | AGAAATTGATGAAAAATGATTAACTTTTCAGGCTAATGATGTGCAATTTAGTGCATGAG  | 1781 |
| Db | 285  | AAAATTGATGAAAAATGATTAACTTTTCAGGCTAATGATGTGCAATTTAGTGCATGAG   | 226  |
| Qy | 1782 | GCACTTAATTT---AGTGTACAATGTCGCAAGTAGTGACTTAAAAAATAATATTGATA   | 1838 |
| Db | 225  | GCAGTAAATTTGGGTGTATCTGTACAGGAATGGTGTGTAACCTAAAAAATAATATTGATA | 166  |
| Qy | 1839 | TGAACCATGCACTCTCTTTGGGG-----AAAAAGTAATGATTAACCTCTTTAGGA      | 1890 |
| Db | 165  | CAAGCAGCAATAGTCTCTTTGGGGGTGTGTGAAGGGAGTAATTAATTAATTTCAAGA    | 106  |
| Qy | 1891 | GTCCTTAGCTTCCCAAAAAGTAGTAGAAAAATAATATCTCTGTGGCCTGGAAACAGTT   | 1950 |
| Db | 105  | CTCTCTAGACTTCCCAACAGGAGGAGAA-----CTGTGGGCTGGAAAGGTCT         | 55   |
| Qy | 1951 | CTGTTTCTTGCGGGCTATATTTGTTAGGTTTTTAATAGTTCATTTGATTAAGACT      | 2006 |
| Db | 54   | CTGTCCCT--GCTGCTGTGTTTGTTCACACTCTTTAAGAGTCAACCCCAATTGATCT    | 1    |

|                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                   |
|---------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------|
|                           | BX971880/c                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                   |
| LOCUS                     | BX971880                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 829 bp DNA linear GSS 05-JUL-2004 |
| DEFINITION                | Forward strand read from insert in 5'HPT insertion targeting.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                   |
| ACCESSION                 | BX971880                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                   |
| VERSION                   | BX971880.1 GI:49703303                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                   |
| SOURCE                    | GSS; genome survey sequence; MICER.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                   |
| ORGANISM                  | Mus musculus (house mouse)                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                   |
| REFERENCE                 | Mus musculus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                   |
| AUTHORS                   | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.<br>1 (bases 1 to 829)<br>Adams,D.J., Baggot,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,<br>Jenkins,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,<br>Rogers,J. and Bradley,A.<br>Direct Submission<br>Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,<br>CB10 1SA, UK. http://www.sanger.ac.uk/MICER<br>Location/Qualifiers<br>1..829<br>/organism="Mus musculus"<br>/mol_type="genomic DNA"<br>/db_xref="taxon:10090"<br>/clone="MHPN10117"<br>/clone_1ib="MHPN" |                                   |
| TITLE                     | JOURNAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |                                   |
| FEATURES                  | source                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |                                   |
| ORIGIN                    |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                   |
| Query Match               | 6.9%; Score 235.2;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | DB 9; Length 829;                 |
| Best Local Similarity     | 68.9%;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Pred.No.5,4e-37;                  |
| Matches 452; Conservative | 0; Mismatches 168;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Indels 36; Gaps 8                 |
| Oy                        | 1370 TTACAAGGCGCAACTGATCTGAACCTCAGGTCTATCCAACTCCAGACCTGGAGTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1423                              |
| Dd                        | 639 TTAGAAGAGGCATAATTGAGTTTGACTCAGGTTTATTGACTCTTCAGTCTCACCTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 580                               |
| Oy                        | 1430 CAATTGCTACACAAATCTTAATCAAGTTAAAAGGAAAAAGATTGATTGCTCAGAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1488                              |
| Dd                        | 579 CAA TGCCAGTAGCTGTA AAAAAAAAAAAAAAAAAAATCAGAGATCA-----ATTTCCTGAGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 524                               |
| Oy                        | 1490 GTATAGGGCATATGTTAC---AATTATTAATTAACAAAGTTATATAGTGA AAAATA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 1541                              |
| Dd                        | 523 ATATAGCACCATGTGTAATGATTAATATGACATCGAAAAGAAATTTATATCAGAAAATGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 464                               |

|    |      |                                                                |      |
|----|------|----------------------------------------------------------------|------|
| Qy | 1547 | ATTATTCGAAACAAATTAACCTTTATTAAGCCTGATCTTAATCTGCTGCGCAACAAAGACTA | 1606 |
| Db | 463  | ATTTTCGAGCAAAATCTGACTTTATTAAGCCTGCTCTTAATATGTCTTGA--TTAAAGG    | 406  |
| Qy | 1607 | TCTGAAATCCCTTCGAGGCGATCTGTGTTGTGTCGTGTTTCCTTAATCTTTAATGATGAGC  | 1666 |
| Db | 405  | GCCAGATCACCTGAGGGGTGTCGTGTTGTGTCGTGTTTCCTTCATCTTTAATGATGAGGC   | 346  |
| Qy | 1667 | AAATCTAATGATTAATGTAAGGCCA-----TTTTTCTCAAGAGATGATGATCTCTTA      | 1721 |
| Db | 345  | AAATCTAGTACATTAATGAAAGCCACTTTTTCCTCAAGAGATTAATGATGCTCTTA       | 286  |
| Qy | 1722 | AGATTTGATGAAATGATCATTTAATCTTTACGCTACTAGTTGCATTTATAGTCAGTACG    | 1781 |
| Db | 285  | AAATTTGATGAAATGATCATTTAATCTTTCAAGTACTAGCTGATCTTTATGTTCACTGAG   | 226  |
| Qy | 1782 | GCAGTAAATT--AGTGTACATGTGGGAAAGTATGTACCTTAAATAATTAATTGATA       | 1838 |
| Db | 225  | GCACTAAATTTGGGTGTATACGTACAGAAATGTGTGACCTTAAATAATTAATTGATA      | 166  |
| Qy | 1839 | TGAACCACTGACTCTCTTGGGG-----AAAAAGTATGATTAACCTCTTAAGA           | 1890 |
| Db | 165  | CAAAGCCACATAGTCTCTTGGGGGTGTGTATAGGGAGTATGAAATTAAATTCATAAGA     | 106  |
| Qy | 1891 | GTCCTTAAGCTTCCCAAAAGTAGAGAAAAATTAATCTCTGTGGGCTCGAAACAGCTT      | 1956 |
| Db | 105  | CTCCTCAAGCTTCCCAAAACAGAGAGAGAA-----CTCTGTGGGCTCGAAACAGCTCT     | 55   |
| Qy | 1951 | CTGTTTCTGTGGCTAATTTGTTTAAAGTATTAATAGTTCATTTGATTAAGACT          | 2006 |
| Db | 54   | CTGTGCTCT--CTGTGTGTTTGTTCAGCTCTTTAAGATTCACCCCAATTGATCT         | 1    |

| LOCUS                 | CR242965/c                                                                                                                                                    | 835 bp                                                       | DNA        | linear      | GSS 06-JUL-2004 |
|-----------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|------------|-------------|-----------------|
| DEFINITION            | Forward strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN355104, genomic survey sequence.                            |                                                              |            |             |                 |
| ACCESSION             | CR242965                                                                                                                                                      |                                                              |            |             |                 |
| VERSION               | CR242965.1                                                                                                                                                    | GI:50021814                                                  |            |             |                 |
| KEYWORDS              | GSS; genome survey sequence; MICER.                                                                                                                           |                                                              |            |             |                 |
| SOURCE                | Mus musculus (house mouse)                                                                                                                                    |                                                              |            |             |                 |
| ORGANISM              | Mus musculus                                                                                                                                                  |                                                              |            |             |                 |
| REFERENCE             | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.                          |                                                              |            |             |                 |
| AUTHORS               | Adams D.J., Biggs P.J., Cox A.V., Davies R.M., van der Weyden L., Rogers J., Smith J., Plumb R.W., Taylor R.G., Nishijima I., Yu Y., Rogers J. and Bradley A. |                                                              |            |             |                 |
| TITLE                 | Direct Submission                                                                                                                                             |                                                              |            |             |                 |
| JOURNAL               | Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <a href="http://www.sanger.ac.uk/MICER">http://www.sanger.ac.uk/MICER</a>       |                                                              |            |             |                 |
| FEATURES              | Location/Qualifiers                                                                                                                                           |                                                              |            |             |                 |
| Source                | 1..835                                                                                                                                                        |                                                              |            |             |                 |
|                       | /organism="Mus musculus"                                                                                                                                      |                                                              |            |             |                 |
|                       | /mol_type="genomic DNA"                                                                                                                                       |                                                              |            |             |                 |
|                       | /db_xref="taxon:10090"                                                                                                                                        |                                                              |            |             |                 |
|                       | /clone_1="MHPN355104"                                                                                                                                         |                                                              |            |             |                 |
|                       | /clone_11b="MHPN"                                                                                                                                             |                                                              |            |             |                 |
| ORIGIN                |                                                                                                                                                               |                                                              |            |             |                 |
| Query Match           | 6.8%;                                                                                                                                                         | Score 231.8;                                                 | DB 9;      | Length 835; |                 |
| Best Local Similarity | 69.2%;                                                                                                                                                        | Ped. No.2.7e-36;                                             |            |             |                 |
| Matches 445;          | Conservative 0;                                                                                                                                               | Mismatches 162;                                              | Indels 36; | Gaps 8      |                 |
| QY                    | 1370                                                                                                                                                          | TTACACAGTGGCAACTGAGATCTGAACCTCAGAGTCTCAACCTCCAGAGACTGGAGATCC | 1422       |             |                 |
| DB                    | 629                                                                                                                                                           | TTTGAAGAGGCAAAATTGAGATTGAACCTCAGAGTTATTGACTCTTCAGTTCAGCTCA   | 570        |             |                 |
| QY                    | 1430                                                                                                                                                          | CAATGCTACACAAATTTCTTATCAAGTTAAAGGAAAAAGGATTGATTGCTCAGAACT    | 148        |             |                 |
| DB                    | 569                                                                                                                                                           | CAATGCAAGTACAGCTTAAAAAATAAATCAGAGATCA-----ATTTCCTGTGAGGT     | 514        |             |                 |







Db 120 -----TTTAAATGATGCAAAACTGCAATGATGTTATATTACCTGTGATGCTGA 175

QY 3347 TTGTTGCTGGCCAGTGGATCTGAATGAAACAGCGAG 3384

Db 176 TTGCTGCTGGCCAGTGGATCTGAATGAAAGGACAGTGGAG 213

RESULT 8  
AQ424198/c 704 bp DNA linear GSS 24-MAR-1999  
LOCUS CITBI-E1-2574F19.TR CITBI-E1 Homo sapiens genomic clone 2574F19,  
DEFINITION genomic survey sequence.  
ACCESSION AQ424198  
VERSION AQ424198.1 GI:4497508  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS Zhao,S., Adams,M.D., Niernan,W., Malek,J., Shizuya,H., Simon,M. and  
Venter,J.C.  
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready  
Map Building  
JOURNAL Unpublished (1997)  
COMMENT Other GSSes: CITBI-E1-2574F19.TF  
Contact: Shaying Zhao, William Niernan, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0208  
Fax: 301 838 0208  
Email: hbe@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/cdb/hungen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.

FEATURES  
source  
Location/Qualifiers  
1..704  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="2574F19"  
/sex="male"  
/cell\_type="sperm"  
/clone\_lib="CITBI-E1"  
/note="Vector: pBelobAC11; Site\_1: EcoRI; Site\_2: EcoRI;  
Caltech Human BAC Library D"

ORIGIN  
Query Match 3.5%; Score 117.4; DB 8; Length 704;  
Best Local Similarity 64.6%; Pred. No. 4.1e-13;  
Matches 223; Conservative 0; Mismatches 116; Indels 6; Gaps 3;

QY 84 AATTATTCAGTGCAGCTCCGGAGATTGGATAGAGCGTCACTCATTTACACAGTGG 143

Db 642 ATTATATGCGAGTACCAAGCTGAGACATTTCACAGTAATATTCATTATTCAGGTG 583

QY 144 TTATGTTTCAACCAATCACTGCCACA-TGAATTAAGTATTCCTGAAACCACTGCCCTAG 202

Db 582 CTAATTTCTATAAAGTCAACCAACACAGCATTTAGCAAAATGACGACATTGTTCTTAG 523

QY 203 GGGAACTACAGGTTAGATTCCTGCTGAGCTCTGCTGACGTTTTTTGTTAAACAATCAATA 262

Db 522 GGGACTACAGGTTAGATTCCTGCTGAGCTCTGCTGACATTTTGTCAACAGATCAATA 463

QY 263 AATAACCTGTTTGTGTCATTTGTTTAAATCTTATTAATTAAGTACGTCGA 322

Db 462 CATTAACCTGTTGATATGTGTTCT-ATTAAAGGACCTTATTTGTAATATGCTTG 404

QY 323 ATTCTTCAACATTTGGTTCACAAACAAAGCCCTTAACTGAAAGCCCTGAATGAAC 382

Db 403 GTTCATTAGTGTAAACACACAGCCAAACAG----CACTATTAAGTCAATGTAACAAAGC 348

QY 383 TTACATACACACATTTGTTTCATGAGGAAATTTTCTTC 427

Db 347 TTATCTACACACATATTTTCTCATTAATGACATCAAGCCCTTC 303

RESULT 9  
AU120374/c 749 bp mRNA linear EST 01-AUG-2002  
LOCUS AU120374 HEMBB1 Homo sapiens cDNA clone HEMBB1000550 5', mRNA  
DEFINITION sequence.  
ACCESSION AU120374  
VERSION AU120374.1 GI:10935609  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 749)  
AUTHORS Oca,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,  
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and  
Isogai,T.  
TITLE HRI human cDNA project  
JOURNAL Unpublished (2000)  
COMMENT Contact: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3975  
Fax: 81-438-52-3986  
Email: genomc@hri.co.jp  
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; cDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES  
source  
Location/Qualifiers  
1..749  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HEMBB1000550"  
/tissue\_type="whole embryo, mainly body"  
/dev\_stage="embryo, 10 weeks"  
/clone\_lib="HEMBB1"  
/note="Vector: pME18FL3"

ORIGIN  
Query Match 3.3%; Score 111.8; DB 1; Length 749;  
Best Local Similarity 68.9%; Pred. No. 5.6e-12;  
Matches 213; Conservative 0; Mismatches 87; Indels 9; Gaps 4;

QY 113 GGTATGAGCTGACTCTATTTATTCACAGTGGTTATGTTCTACCCAAATGACGCAACG-T 171

Db 553 GGATACAGTCCATCTCTCATTTATTTGTAGTATTAATGTTCCATTAAGTTCACACACAGT 494

QY 172 GAATAGATTTCTGCAACCACTGCCCTAGAGGGAATACAAAGTTAGATTCCTGTCAGC 231

Db 493 GAAAGTGAATATCTGAACCTATGCTCTTAGGGGAAATACAGATTTAGATTCCTGTAAC 434

QY 232 CTCGTG--TCAAGTTTGTGTTAAACCAATCAATAATTAACCTGTTTGTGTCATTTCT 288

Db 433 CTCGTGCTACCAACATTTTGTCAACCAATCAATACATATAGCTGTTTATGTTGTTTCT 374

QY 289 GTTTTAAATATCTTTATTTATATAGTACTGTATTTCTTCAACATTTTGTTTCAACCA 348

Db 373 GTTTCAGA-CTCCTTATTTATTAATTAATTTGTGATTCATCACTTAAGTCAAGCA 315

QY 349 AAAGCCCTATTTAATGAAAGCCCTGAATGAAGTTTACATACACACATGTTTCTAT 408

Db 314 ACAG---CACTACAGCCCAAGCCGTAAACAAACTTATTTAAACATGATATTTTCTGT 259

QY 409 GAGGAAAAA 417

Db 258 AAAGCACAA 250

RESULT 10  
CNS00EVL/C  
1000000

|            |                                                               |         |     |        |                 |
|------------|---------------------------------------------------------------|---------|-----|--------|-----------------|
| LOCUS      | CNS00EVL                                                      | 1101 bp | DNA | linear | GSS 04-JUN-1999 |
| DEFINITION | Drosophila melanogaster genome survey sequence T7 end of BAC: |         |     |        |                 |

BACK29B23 of RPCI-98 library from *Drosophila melanogaster* (fruit fly), genomic survey sequence.

|            |            |
|------------|------------|
| AL069706   | GI:4949849 |
| AL069706.1 |            |
| CC         |            |

| SOURCE | ORGANISM                                   |
|--------|--------------------------------------------|
| GSS.   | <i>Drosophila melanogaster</i> (fruit fly) |
|        | <i>Drosophila melanogaster</i>             |

ORGANISM  
Eukaryota Metazoa  
Eukaryota Metazoa; Hexapoda; Insecta; Pterygota  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota  
Neometa; Endopterygota; Diptera; Prochirona; Muscophila

1 (bases 1 to 1101)

Genoscope - Centre National de Séquençage :  
Submitted (02-JUN-1999)  
Direct Submission  
AUTHORS  
TITLE  
JOURNAL

| FEATURES | Location/Qualifiers |
|----------|---------------------|
| source   | 1. .1101            |

**ORIGIN**

|                       |                   |                    |           |              |
|-----------------------|-------------------|--------------------|-----------|--------------|
| Query Match           | 3.2%              | Score 107.8;       | DB 9,     | Length 1101, |
| Best Local Similarity | 35.4%             | Pred. No. 3.7e-11, |           |              |
| Matches 224,          | Conservative 126, | Mismatches 278,    | Indels 5, | Gaps 2,      |

[illegible][illegible]

Db 1034 TTAMTTTAAAAATATAMWTTAAATAAATATATMTAMTAAWATATATAMATAMAAATATATAW 975

D6  
974 AATTGAAATGAATTAATAAATAATGTTTCTTTTTTTTTTTT 915

QY 2487 AACCTAATACTAGTCAMTGGAACTGAAATACAAATTTTCATATGATATAAAGATATTATT 2546

2547 TAAAGTATTCATGAGCAATTATATTAAAGTAGAATTTTCATTATGTTAGAAAT 2608

Dd 857 MATTTTITWTATTTWTAATAAATWTAATWTTTAAATWTAATATTATATATWTTT 798

2607 TTAATCAGGGAAACAAGTTTCTCAATTATAGAGAAATCTTTACTAGTATACAGTC 2666

DB 79 T W I A I T W I A I T A M M M M T W A T M M M I A A M M I A T A T A M M W A I T A T A T W M T W I A T W I T W I T 738

QY 2667 T T T T C A T T T A G C T C T C G A A T P A A F C T G I A T T T T C T A A T T A T A C A A G A C T A A A A T P A 21268

Db 737 TTAATTTTAAATTATATATAATTTTATWATTTTTTTTTTTTTTTTAAATTTAAATA 678

QY 212 TTTTAAATACCAATAA--AAATTATTTTACTTCCTTAAGTAAAAT 2784  
||||| : : ||||| : ||||| : ||||| : ||||| :  
Db 677 TTATAATTMMWALTWMTTATTATAATAWTAAATTAATTTAAAAA 618

QY 2785 CATTATATTTCTGAGGNAACATATCACTTTTAAGTATGAAAGTAAATTAGAT 2844

2845 TTATTCACCTAATTATATTTTAAAGTTTCACATATAAAGATGAATGAAGATCTAAGC 2904  
 62 TATTTTTTAAATATATATATATATATATATATATATATATATATATATATATATAT 538  
 63 TATTTTTTAAATATATATATATATATATATATATATATATATATATATATATATAT 539

Db 557 WTTTAAATATATTTTTTTTTTTTAAATWAAWTTWAAAATAWAAAAATWAAAAATWTTT 498

497 TTWATTWATAAATTTTWTTTWMAATTTWKKKK 465

RESULT 11  
BOENE /

|            |                    |                      |               |                 |
|------------|--------------------|----------------------|---------------|-----------------|
| LOCUS      | 571 bp             | DNA                  | linear        | GSS 26-JUN-1998 |
| DEFINITION | B95505             |                      |               |                 |
|            | CIT-HSP-2165E24.TF | CIT-HSP Homo sapiens | genomic clone | 2165E24,        |
|            | Genomic            | survival             | sequence      |                 |

Genetic survey sequence.  
ACCESSION B95505  
VERSION B95505.1 GI:2977842  
KEYWORDS GSS.

**SOURCE ORGANISM**  
Homo sapiens (human)  
Homo sapiens  
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Rura]eostomi:

REFERENCE  
1 (bases 1 to 571)  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
Adams, M.D., Rounslev, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K.

| TITLE                                                                                             | Author                                                           |
|---------------------------------------------------------------------------------------------------|------------------------------------------------------------------|
| Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M., and Venter, J. C. | Use of a random BAC End Sequence Database for Sequence-Ready Map |

Building (1998)  
Unpublished (1998)  
Other GSSs: CIT-HSP-2165B24.TR  
JOURNAL  
COMMENT

Contact: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208

Email: [mdadams@tigr.org](mailto:mdadams@tigr.org)  
Clones are available from Research Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC  
end search page:

http://www.tigr.org/cdb/humgen/bac\_end\_search/bac\_end\_search.html  
Seq primer: M13-21;  
Class: BAC ends.

```
FEATURES
source
location/Qualifiers
1..571
/Organism="Homo sapiens"
```

```

/mol_type="genomic DNA"
/db_xref="GDB:7101106"
/db_xref="taxon:9606"

```

```

      /clone="2165E24"
      /sex="Male"
      /cell_type="Sperm"

```

```

/clone_id="C11-HSp"
/notes="Vector: pBelobAC11, site_1: HindIII, site_2:
HindIII"

```

| Query Match | Score | DB | Length |
|-------------|-------|----|--------|
| 3.2%        | 107.4 | 8  | 571    |
| 70.6%       | 107.4 | 8  | 571    |

Matches 173; Conservative 0; Mismatches 71; Indels 3; Gaps 2;

QY 115 ATGAGCTGCTCTCTATTATTCACAGTGTATTTCTTACCATCTGCGCAAC-TGA 173  
 |||||  
 Db 318 ATACAGACATTCATATTAATTCATCGATGATATCTCTGTAAGTCTGCAACACTGA 259  
 174 ATAGATATCCCTAACCACTGCGCCCTAGGGGAACCTCAAGGTAGATCCCGTCAAGCT 233  
 258 ATTAGTAAATCTAGACCATCTGCTCTAGAGAAACAGGGTTAAGTCTGCGACCT 199  
 Db 234 CTGTCACGTTTTTGTAAACCAATCAATTAATACCTGT--TTGTGTGCAATTTCTGT 291  
 198 CTGTGCGCAATTTATCAAGCTTCAATACATTAATCTTCTCTAGTGTGTTTTTGT 139  
 QY 292 TTAATAATCTTTATTTATACGTAAGCTTAATTTCTCAATTTGGTTCACACCAAAA 351  
 |||||  
 Db 138 TTAAGACACCTTATTAACATGATATTTTGTATGATTAAGCTTGAACTCAGCCAAA 79  
 QY 352 GGCCCTA 358  
 |||||  
 Db 78 TGCTATA 72

RESULT 12  
 LOCUS AO729830 440 bp DNA linear GSS 15-JUL-1999  
 DEFINITION HS\_5430\_A1-B09-T7A-RPCT-11 Human Male BAC Library Homo sapiens  
 genomic clone Plate=1006 Col=17 Row=C, genomic survey sequence.

ACCESSION AO729830  
 VERSION AO729830.1 GI:5501382  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 440)  
 Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,  
 Mahairas G.G., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and  
 Hood L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 MEDLINE 99380589  
 PUBMED 10449764

COMMENT Contact: Mahairas G.G., Wallace J.C., Hood L.  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887

Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCT-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.hsc.washington.edu

Seq primer: T7  
 Plate: 1006 Row: C Column: 17  
 Class: BAC ends  
 High quality sequence stop: 440.

#### FEATURES

source location/Qualifiers  
 1..440  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=1006 Col=17 Row=C"  
 /sex="male"  
 /clone\_11b="RPCT-11 Human Male BAC Library"  
 /note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 Male blood DNA was isolated from one randomly chosen donor  
 and partially digested with a combination of EcoRI and  
 EcoRI Methylase. Size selected DNA was cloned into the

ORIGIN pBAC3.6 vector at EcoRI sites"

Query Match 3.2%; Score 107.2; DB 8; Length 440;  
 Best Local Similarity 65.5%; Pred. No. 4.6e-11;  
 Matches 190; Conservative 0; Mismatches 93; Indels 7; Gaps 2;

QY 124 ACTCTCATTTATTCACAGTGTATGTTCTTACCCATCTACGCAACATGAAATAGATT 183  
 |||||  
 Db 4 ATTCTCATTTATTCAGTGTATGTTCTTATGTTAGTCACTACAAACCTGAATTGCAAT 63

QY 184 CTGAACCACTGCCCTTAGGGAACTACAGGTTAGTTCCCTGACCTTGGTCA-- 241  
 |||||  
 Db 64 ACTGAATGATGGCCTTAGGGGAAATACAGATGAGCTCTGAGACCTCTGGTCAAA 123

QY 242 -GTTTTGTAAACAATCAATTAATACCTGTTTGTGCAATTTGTTTAAATAT 300  
 |||||  
 Db 124 TATTTGTCAACGATCAATTAATTAACCTAGTTTATATGTTTCTGCTAAAGACAC 183

QY 301 CTATTATTAATACGTAAGCTTAATTTCTCAACATTTGTTTCAACAAAGGCTTATT 360  
 |||||  
 Db 184 CTCTTCAATTAATTAATTTGATTTACTTAACATTAATCAATGACCAACAG---CACT 239

QY 361 AACTGAAGCCCTGATGATGAGCTTACATTAACACATTTGTTTCTATGA 410  
 |||||  
 Db 240 GTCACTTATGCTGTAAGAAAGCTATCTTAATTAACAGATATTTTCTAGA 289

RESULT 13  
 LOCUS CC118439 987 bp DNA linear GSS 16-APR-2003  
 DEFINITION NDL\_83G12\_SPE Nctre Dame Liverpool Aedes aegypti genomic clone  
 NDL\_83G12, genomic survey sequence.

ACCESSION CC118439  
 VERSION CC118439.1 GI:29987494  
 KEYWORDS GSS.  
 SOURCE Aedes aegypti (yellow fever mosquito)  
 ORGANISM Aedes aegypti  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;

REFERENCE 1 (bases 1 to 987)  
 Loftus B., Shetty U., Knudson D. and Severson D.

TITLE BAC end sequencing of Aedes aegypti  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: NDL\_83G12..T7

Contact: Brendan Loftus  
 Department of Eukaryotic Genomics  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-3543  
 Fax: 301-838-0208

Email: entae@tigr.org  
 Library was provided by David Severson  
 Seq primer: SP6  
 Class: BAC ends.

#### FEATURES

source location/Qualifiers  
 1..987  
 /organism="Aedes aegypti"  
 /mol\_type="genomic DNA"  
 /strain="Liverpool"  
 /db\_xref="taxon:7159"  
 /clone="NDL\_83G12"  
 /clone\_11b="Nctre Dame Liverpool"  
 /note="Vector: pBAC3.1; Site\_1: Hind III; The library was  
 prepared from whole body tissue of newly hatched 1st larvae  
 by David Severson at the University of Nctre Dame and  
 Hongbin Zhang"

ORIGIN  
 Query Match 3.1%; Score 106.4; DB 8; Length 987;  
 Best Local Similarity 66.2%; Pred. No. 7.1e-11;  
 Matches 217; Conservative 0; Mismatches 101; Indels 10; Gaps 4;



QY 109 GATTGATAGAGCTGACTCTCATTTATTCACAGTGGTTATGTTTCAACCAATCATCTGCCAA 168  
 DB 251 GTTGGAAATACAGCTGATTCATTCATTTTTCAGTAGTCTTCTGTAAAGTACACAGGAA 310  
 QY 169 C-ATGAAATAGATTTCTGTAACCACTGCCCCCTAGGGGAATCAAGAGTTAGATTCCTGT 227  
 DB 311 CGCTGAATTTAACTAAATTTGAACTCTTCTCCCAAGAAATAGGGGTGAGTTCTCTGC 370  
 QY 228 CAGCCTCTGTCTAC---GTTTTGTAAACCAATCAATTAATTAACCTTGTGTTGTGCA 283  
 DB 371 AGGCTCTGTCTACCAACTTTTGTGATCATATTAATTAATTAATTTGTTATGTTT 430  
 QY 284 TTTCTGTTTAAATATCTTATTTATATACGTACTGTAATTTCTTCAACATTTGTTGAC 343  
 DB 431 TTTCTGTTTAAAGACA-CCTTATGTAATACATCTTGTGATTTCAATTAATTAAGACTCAC 489  
 QY 344 AACCAAAAGCCCTTTTAACTGGAAGCCCTGATGATGAGCTTACATTAACACATTTGTTT 403  
 DB 490 AGCCAAATAG---CACTGTAACTCATCTGATGATGACATATTAACACAGTATTTTC 545  
 QY 404 TCTATGAGGAAATTTTCTCTGAGTC 431  
 DB 546 TCTGGAGGCAATCAACAGCTTCTTTC 573

RESULT 14  
 A0120350 487 bp DNA linear GSS 22-SEP-1998  
 LOCUS HS\_3010\_B2\_B01\_T7 CIT Approved Human Genomic Sperm Library D Homo  
 DEFINITION sapiens genomic clone Plate=3010 Col=2 Row=D, genomic survey  
 sequence.

ACCESSION A0120350  
 VERSION A0120350  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 487)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
 Hood,L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

TITLE Contact: Mahairas GG, Wallace JC, Hood L  
 JOURNAL High Throughput Sequencing Center  
 MEDLINE University of Washington  
 PUBMED 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 10449764  
 99380589

COMMENT Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Sequence Tagged Connector  
 Plate: 3010 row: D column: 2  
 Class: BAC ends  
 High quality sequence stop: 487.  
 Location/Qualifiers

FEATURES  
 source  
 1. 487

/organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=3010 Col=2 Row=D"  
 /sex="male"  
 /clone\_lib="CIT Approved Human Genomic Sperm Library D"  
 /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in  
 E-Coli DH10B"

ORIGIN  
 Query Match 3.1%; Score 104; DB 8; Length 487;  
 Best Local Similarity 61.5%; Pred. No. 2.1e-10;

Matches 201; Conservative 0; Mismatches 121; Indels 5; Gaps 2;  
 QY 121 CTGACTCATTAATTCACAGTGGTTATGTTTCAACCAATCATCTGCCAAATGAATG 180  
 DB 16 CTGGACATTCATTTTCTCGATGATTAATTCACANAGTTGCCAACAACATGATAGCT 75  
 QY 181 ATTCCTGAACCACTGCCCCCTAGGGGAATCAAGAGTTAGATTCCTGAGCTCTGTCA 240  
 DB 76 TATACGAACTTATGATCTTAAGGAATTAAGGGTATGCTCTTGCAAGCTTATGTC 135  
 QY 241 CGTTTTGTAAACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 300  
 DB 136 CATCTGTGCAACAATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 194  
 QY 301 CTTATTTAATACGTAAGTCTTAATTTCTTCAACATTTGTTTCAACAAAGGCCCTATT 360  
 DB 195 CTTATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 250  
 QY 361 AACTGAAAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
 DB 251 AGAGGAGATGACTTCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 310  
 QY 421 TTCCTTCACTCTGCGCAAGCTTCTT 447  
 DB 311 TGTGATTAAGAAATGCAATGATGATGCTT 337

RESULT 15  
 AG124176/c 624 bp DNA linear GSS 04-NOV-2001  
 LOCUS AG124176 Pan troglodytes DNA, clone: PTB-134A20.R, genomic survey sequence.

ACCESSION AG124176  
 VERSION AG124176.1 GI:1665341  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.  
 1  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Torok,Y., Watanabe,H. and Sakaki,Y.  
 BAC end sequences of library PTB  
 Unpublished  
 2 (bases 1 to 624)

TITLE Direct Submission  
 JOURNAL Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC),  
 1-7-22 Suehiro-cho,Tsukumi-Ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:chimbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end  
 was generated during the R&D process and may have higher chance of  
 clone tracking errors.

COMMENT PRIMER  
 Sequencing: M13Rev  
 LIBRARY Vector : PKS145  
 R.Site 1 : SacI  
 R.Site 2 : SacI

FEATURES  
 source  
 1. 624

/organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-134A20.R"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC Library"

ORIGIN  
 Query Match 3.1%; Score 103.4; DB 9; Length 624;

Best Local Similarity 66.5%; Pred. No. 2.8e-10;  
Matches 163; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

|    |     |                                                             |     |
|----|-----|-------------------------------------------------------------|-----|
| QY | 66  | ATTCTTGGAGTACCTCTTAATTCATTCAATGCTGACCTCCGAGATTGGATAGAGCTGAC | 125 |
|    |     |                                                             |     |
| Db | 361 | ATCTGTTGTCATACAGCCATCTTTCACCTCCAGAGTATTTTATTAATAGAGCTAT     | 302 |
|    |     |                                                             |     |
| QY | 126 | TCTCATATCAAGAGTGTATGTTCTACCAATCACTGACCAATG-AATTAAGTATTC     | 184 |
|    |     |                                                             |     |
| Db | 301 | TCTTTTATGACAGTATGTTTATTAATTCATCTGCAACACCAATTTGGTGAATA       | 242 |
|    |     |                                                             |     |
| QY | 185 | CTGAACCACTGCCCCCTAGGGGAACTACAGGTAGATTCCCGTACGCTGTGACGTT     | 244 |
|    |     |                                                             |     |
| Db | 241 | CTGAACTATCACTCTAGGGGAAACATAGGTGAGTTCTGCAAGGCTGTGATACATT     | 182 |
|    |     |                                                             |     |
| QY | 245 | TTTGTTAACCAATCAATTAATTAACCTGTTTGTGTGATTTCTGTTTAAATATCTTT    | 304 |
|    |     |                                                             |     |
| Db | 181 | TTTATCAACCAATCAATTAATTAACCTGTTTGTGTGATTTCTGTTTAAAGACACCTTA  | 122 |
|    |     |                                                             |     |
| QY | 305 | ATTTA                                                       | 309 |
|    |     |                                                             |     |
| Db | 121 | TTTAA                                                       | 117 |

Search completed: March 31, 2005, 14:38:27  
Job time : 6904 secs